

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_23617338_f1_66	3435	7207	528	175	215	1.2e-24

Description

sp:[LN:YAGU_ECOLI] [AC:P77262] [GN:YAGU] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 23.0 KD PROTEIN IN INTF-EAEH INTERGENIC REGION] [SP:P77262]
 [DB:swissprot] >pir:[LN:G64754] [AC:G64754] [PN:probable membrane protein
 yagU] [GN:yagU] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1657488]
 [LN:ECU73857] [AC:U73857] [OR:Escherichia coli] [DB:genpept-bct1]
 [DE:Escherichia coli chromosome minutes 6-8.] [NT:hypothetical protein]
 [LE:10789] [RE:11403] [DI:direct] >gp:[GI:g1786481] [LN:AE000136]
 [AC:AE000136:U00096] [PN:orf, hypothetical protein] [GN:yagU] [FN:orf;
 Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12
 MG1655 section 26 of 400 of the completegenome.] [NT:o204; 26 pct identical
 to 46 residues of approx.] [LE:7372] [RE:7986] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_23621010_c1_971	3436	7208	843	280	167	1.5e-10

Description

pir:[LN:E69777] [AC:E69777] [PN:transcription regulator AraC/XylS family
 homolog ydeC] [GN:ydeC] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1020103:g1881323] [LN:AB001488] [AC:AB001488] [GN:ydeC]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of
 the regionbetween 35 and 47 degree.] [NT:PROBABLE HTH_ARAC_FAMILY OF
 TRANSCRIPTIONAL] [LE:94733] [RE:95608] [DI:complement]
 >gp:[GI:e1182481:g2632815] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeC]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
 transcriptional regulator (AraC/XylS] [LE:158478] [RE:159353]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_23626000_f2_582	3437	7209	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_23629040_c2_1318	3438	7210	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23631928_f2_520	3439	7211	228	75		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23634651_c1_964	3440	7212	1044	347	549	5.0e-53
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Description

pir:[LN:H70000] [AC:H70000] [PN:two-component sensor histidine kinase homolog ytsB] [GN:ytsB] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185912:g2635523] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to two-component sensor histidine kinase] [LE:113501] [RE:114505] [DI:complement] >gp:[GI:g2293176] [LN:AF008220] [AC:AF008220] [PN:signal transduction protein kinase] [GN:ytsB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:65922] [RE:66926] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23672137_c2_1196	3441	7213	957	318	260	6.6e-32
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Description

pir:[LN:S76964] [AC:S76964] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
>gp:[GI:d1019609:g1653966] [LN:D90917] [AC:D90917:AB001339] [PN:47 kD protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470.] [NT:ORF_ID:slr0609] [LE:151573] [RE:152724] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23672562_c1_924	3442	7214	297	98	86	0.0034
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Description

gp:[GI:e8900:g1335718] [LN:PFRESAR1] [AC:X05182] [PN:ring-infected erythrocyte surface antigen] [GN:RESA] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P.falciparum FC27 Ag46 RESA mRNA for ring-infected erythrocytesurface antigen.] [SP:P13830] [LE:<1] [RE:>955] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23703750_c1_1095	3443	7215	639	212		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23728412_c3_1509	3444	7216	699	232	726	8.7e-72
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Description

pir:[LN:C70020] [AC:C70020] [PN:conserved hypothetical protein yusB]
 [GN:yusB] [CL:probable transport protein yaeE] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1184352:g2635770] [LN:BSUB0017] [AC:Z99120:AL009126]
 [GN:yusB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 17 of 21): from 3197001to 3414420.]
 [NT:similar to hypothetical proteins] [LE:164664] [RE:165332]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23844575_c2_1274	3445	7217	1062	353	1442	1.2e-147
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Description

gp:[GI:e1393153:g4490612] [LN:SAU133520] [AC:AJ133520] [PN:gap regulator]
 [GN:gapR] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus
 aureus gap operon (gapR, gap, pgk and tpi genes).] [LE:779] [RE:1792]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23984775_f1_83	3446	7218	153	50		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_23989061_f2_399	3447	7219	138	45		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_2401430_c3_1473	3448	7220	762	253	1076	7.1e-109

Description

gp:[GI:e1387399:g4379428] [LN:SAAJ3781] [AC:AJ223781] [PN:thioredoxin reductase] [GN:trxB] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:1.6.4.5] [DE:Staphylococcus aureus trxB gene.] [LE:1262] [RE:2197] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24022582_f2_316	3449	7221	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24033567_c2_1316	3450	7222	450	149	207	8.6e-17

Description

pir:[LN:G70023] [AC:G70023] [PN:hypothetical protein yutE] [GN:yutE] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184309:g2635727] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:120886] [RE:121320] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24218785_c2_1275	3451	7223	1047	348	1597	4.4e-164

Description

gp:[GI:e1393154:g4490613] [LN:SAU133520] [AC:AJ133520] [PN:glyceraldehyde-3-phosphate dehydrogenase] [GN:gap] [FN:transferrin binding protein] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes).] [NT:putative] [LE:1845] [RE:2855] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24230001_f2_362	3452	7224	258	85		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24240888_f1_281	3453	7225	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24242285_c3_1516	3454	7226	1056	351	439	2.2e-41

Description

gp:[GI:g4981378] [LN:AE001751] [AC:AE001751:AE000512] [PN:hemolysin-related protein] [GN:TM0845] [OR:Thermotoga maritima] [DB:genpept-bct2]
[DE:Thermotoga maritima section 63 of 136 of the complete genome.]
[NT:similar to GB:AE000783 percent identity: 61.61;] [LE:5310] [RE:6677]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24251500_f2_416	3455	7227	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24253153_f1_150	3456	7228	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24256287_c2_1260	3457	7229	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24258388_c3_1405	3458	7230	507	168	102	0.0053

Description

gp:[GI:e1407794:g4493938] [LN:PFMAL3P5] [AC:AL034556] [GN:MAL3P5.10]
[OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
[DB:genpept-inv1] [DE:Plasmodium falciparum MAL3P5, complete sequence.]
[NT:predicted using hexExon; MAL3P5.10 (PFC0620w),] [LE:46925] [RE:48919]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24259762_f3_679	3459	7231	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24266888_c3_1413	3460	7232	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24272125_c2_1292	3461	7233	261	86	72	0.024

Description

gp:[GI:g942589] [LN:MIU29676] [AC:U29676:X55271] [PN:unknown] [OR:Mycoplasma iowae] [DB:genpept-bct2] [DE:Mycoplasma iowae 16S rRNA gene, complete sequence, and 23S rRNA gene, partial sequence.] [LE:<1] [RE:438] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24297000_f2_548	3462	7234	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24329053_c1_979	3463	7235	444	147	142	2.8e-09

Description

gp:[GI:g3329623] [LN:CELF36H12] [AC:AF078790] [GN:F36H12.3] [OR:Caenorhabditis elegans] [DB:genpept-inv2] [DE:Caenorhabditis elegans cosmid F36H12.] [NT:coded for by C. elegans cDNA CEMSF30F] [LE:21606:21872:22500:22677] [RE:21701:22454:22629:22875] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24335801_c2_1326	3464	7236	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24345257_f3_652	3465	7237	168	55		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24347175_c3_1416	3466	7238	165	54		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24391937_c1_1068	3467	7239	759	252	105	0.0062
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Description

pir:[LN:E70031] [AC:E70031] [PN:hypothetical protein yvcD] [GN:yvcD]
 [CL:tetratricopeptide repeat homology] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1186169:g2635994] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcD]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 18 of 21): from 3399551to 3609060.] [LE:175675]
 [RE:177129] [DI:complement] >gp:[GI:e313021:g1945645] [LN:BSZ94043]
 [AC:Z94043] [PN:hypothetical protein] [GN:yvcD] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).] [LE:4542]
 [RE:5996] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24397952_c1_1067	3468	7240	681	226	119	0.00011
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Description

pir:[LN:E70031] [AC:E70031] [PN:hypothetical protein yvcD] [GN:yvcD]
 [CL:tetratricopeptide repeat homology] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1186169:g2635994] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcD]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 18 of 21): from 3399551to 3609060.] [LE:175675]
 [RE:177129] [DI:complement] >gp:[GI:e313021:g1945645] [LN:BSZ94043]
 [AC:Z94043] [PN:hypothetical protein] [GN:yvcD] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).] [LE:4542]
 [RE:5996] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24406577_c3_1415	3469	7241	390	129		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24407637_f1_57	3470	7242	243	80		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24415930_f2_310	3471	7243	1068	355	977	2.2e-98
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Description

pir:[LN:D70024] [AC:D70024] [PN:NADH dehydrogenase homolog yutJ] [GN:yutJ]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184299:g2635717] [LN:BSUB0017]
 [AC:Z99120:AL009126] [GN:yutJ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
 from 3197001to 3414420.] [NT:similar to NADH dehydrogenase] [LE:110924]
 [RE:111916] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_24429650_c3_1408	3472	7244	1197	398	848	1.0e-84
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Description

sp:[LN:NAGA_BACSU] [AC:O34450] [GN:NAGA] [OR:BACILLUS SUBTILIS]
 [EC:3.5.1.25] [DE:DEACETYLASE)] [SP:O34450] [DB:swissprot] >pir:[LN:A69664]
 [AC:A69664] [PN:N-acetylglucosamine-6-phosphate deacetylase nagA] [GN:nagA]
] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186189:g2636014] [LN:BSUB0018]
 [AC:Z99121:AL009126] [PN:N-acetylglucosamine-6-phosphate deacetylase]
 [GN:nagA] [FN:N-acetyl glucosamine utilization] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:3.5.1.25] [DE:Bacillus subtilis complete genome
 (section 18 of 21): from 3399551to 3609060.] [SP:O34450] [LE:194866]
 [RE:196056] [DI:direct] >gp:[GI:g2618856] [LN:AF017113] [AC:AF017113]
 [PN:N-acetylglucosamine 6-P deacetylase] [GN:nagA] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.]
 [LE:31777] [RE:32967] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AR7503001001_24479842_c1_1106	3473	7245	558	185	256	5.5e-22

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pir:[LN:D69800] [AC:D69800 ] [PN:conserved hypothetical protein yfhC]
[GN:yfhC ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182838:g2633172]
[LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhC] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
of 21): from 802821 to1011250.] [NT:similar to hypothetical proteins]
[LE:120274] [RE:120858] [DI:direct] >gp:[GI:d1025385:g2804533] [LN:D85082]
[AC:D85082] [PN:YfhC] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81
degree region.] [LE:13165] [RE:13749] [DI:direct]

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AI7503001001_24490676_c2_1179	3474	7246	141	46
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NO-HIT

AI7503001001_24506712_c2_1240	3475	7247	975	324	879	5.3e-88
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gp:[GI:e1330453:g3724156] [LN:SAA005352] [AC:AJ005352] [PN:membrane protein]
[GN:ssstB] [FN:iron transport] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus, Sst putative iron transport operon.] [LE:1451]
[RE:2132] [DI:direct]
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AI7503001001_24507932_c1_1027	3476	7248	600	199	322	5.6e-29
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pir:[LN:D69924] [AC:D69924 ] [PN:hypothetical protein yorS] [GN:yorS ]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185499:g2634420] [LN:BSUB0011]
[AC:Z99114:AL009126] [GN:yorS] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21):
from 2000171to 2207900.] [LE:172005] [RE:172523] [DI:complement]
>gp:[GI:g3025618] [LN:AF020713] [AC:AF020713] [PN:unknown] [GN:yorS]
[OR:Bacteriophage SPBc2] [DB:genpept-phg] [DE:Bacteriophage SPBc2 complete
genome.] [LE:112997] [RE:113515] [DI:direct]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24611512_c2_1139	3477	7249	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24616050_f2_445	3478	7250	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24640828_c2_1138	3479	7251	516	171		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24642632_f3_765	3480	7252	1245	414	1245	8.7e-127

Description

sp:[LN:PEPT_BACSU] [AC:P55179] [GN:PEPT] [OR:BACILLUS SUBTILIS]
 [EC:3.4.11.-] [DE:PEPTIDASE T, (AMINOTRIPEPTIDASE) (TRIPETIDASE)]
 [SP:P55179] [DB:swissprot] >pir:[LN:H69674] [AC:H69674]
 [PN:aminotripeptidase,:peptidase T] [GN:pepT] [OR:Bacillus subtilis]
 [EC:3.4.11.-] [DB:pir2] >gp:[GI:e254163:g1429259] [LN:BSGALE] [AC:X99339]
 [GN:pepT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis orfs 1,2,3,4, pepT and gale genes.] [SP:P55179] [LE:5267]
 [RE:6499] [DI:direct] >gp:[GI:e1186391:g2636427] [LN:BSUB0020]
 [AC:Z99123:AL009126] [PN:peptidase T (tripeptidase)] [GN:pepT] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [EC:3.4.11.-] [DE:Bacillus subtilis complete
 genome (section 20 of 21): from 3798401to 4010550.] [SP:P55179] [LE:195467]
 [RE:196699] [DI:direct] >gp:[GI:d1012379:g1783235] [LN:D83026]
 [AC:D83026:D45911] [GN:pepT] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:BGSC 1A1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome
 sequence covering lic-cel region.] [NT:highly homologous to tripeptidases
 (peptidase T)] [LE:27766] [RE:28998] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24796927_f1_61	3484	7256	789	262	325	2.7e-29

Description

pir:[LN:E69883] [AC:E69883] [PN:phage-related replication protein homolog ymaC] [GN:ymaC] [CL:phage-related replication protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183386:g2634111] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ymaC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [NT:similar to phage-related protein] [LE:81490] [RE:82197] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24803125_c1_993	3485	7257	978	325	982	6.5e-99

Description

sp:[LN:MDH_BACIS] [AC:Q59202] [GN:MDH] [OR:BACILLUS ISRAELI] [EC:1.1.1.37] [DE:MALATE DEHYDROGENASE,] [SP:Q59202] [DB:swissprot] >pir:[LN:S61213] [AC:S61213] [PN:malate dehydrogenase,] [CL:L-lactate dehydrogenase] [OR:Bacillus israeli] [EC:1.1.1.37] [DB:pir2] >gp:[GI:g963019] [LN:BIDNAMD] [AC:X90527] [PN:malate dehydrogenase] [OR:Bacillus israeli] [DB:genpept-bct1] [EC:1.1.1.37] [DE:B.israeli DNA for malate dehydrogenase gene.] [SP:Q59202] [LE:291] [RE:1229] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_24803332_c2_1305	3486	7258	840	279	712	2.6e-70

Description

pir:[LN:B70020] [AC:B70020] [PN:conserved hypothetical protein yusA] [GN:yusA] [CL:lipoprotein-28] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184351:g2635769] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins] [LE:163826] [RE:164650] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_2531500_c3_1360	3487	7259	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_25401377_c1_1045	3488	7260	852	283	939	2.3e-94

Description

gp:[GI:e1330454:g3724157] [LN:SAA005352] [AC:AJ005352] [PN:ATP binding protein] [GN:SstC] [FN:iron transport] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus, Sst putative iron transport operon.] [LE:2186] [RE:2947] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_25401675_c2_1319	3489	7261	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_25415802_c1_1102	3490	7262	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_25473782_c3_1498	3491	7263	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_25492312_f1_302	3492	7264	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_25572180_c1_956	3493	7265	1272	423	895	1.1e-89

Description

sp:[LN:YXJA_BACSU] [AC:P42312] [GN:YXJA:N15HR] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 43.7 KD PROTEIN IN KATB 3'REGION] [SP:P42312]
[DB:swissprot] >pir:[LN:G70078] [AC:G70078] [PN:pyrimidine nucleoside
transport homolog yxjA] [GN:yxjA] [CL:pyrimidine nucleoside transport
protein nupC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186401:g2636437]
[LN:BSUB0020] [AC:Z99123:AL009126] [GN:yxjA] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
20 of 21): from 3798401to 4010550.] [NT:similar to pyrimidine nucleoside
transport] [SP:P42312] [LE:206141] [RE:207334] [DI:direct]
>gp:[GI:e1184627:g2636448] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yxjA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 21 of 21): from 3999281to 4214814.] [NT:similar to
pyrimidine nucleoside transport] [SP:P42312] [LE:5261] [RE:6454] [DI:direct]
>gp:[GI:d1012369:g665999] [LN:D83026] [AC:D83026:D45911] [GN:yxjA]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genome sequence covering lic-cel
region.] [NT:homologous to pyrimidine nucleoside transport] [LE:17131]
[RE:18324] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_25585891_c2_1218	3494	7266	1980	659	1949	2.2e-201

Description

pir:[LN:D69815] [AC:D69815] [PN:conserved hypothetical protein yfnI]
[GN:yfnI] [CL:Bacillus subtilis probable anion-binding protein yflE]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182705:g2633039] [LN:BSUB0004]
[AC:Z99107:AL009126] [GN:yfnI] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
from 600701 to813890.] [NT:alternate gene name: yetP; similar to
hypothetical] [LE:195080] [RE:197041] [DI:direct] >gp:[GI:d1020933:g2116767]
[LN:D86418] [AC:D86418] [PN:YfnI] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic
DNA 69-70 degree region, partialsequence.] [LE:16150] [RE:18111]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_25806300_f1_275	3495	7267	750	249	1270	2.0e-129

Description

gp:[GI:e255626:g1617428] [LN:SEABCTS] [AC:X99127] [PN:ATP binding protein]
[FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis]
[DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.]
[LE:41] [RE:787] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_26171927_c2_1246	3496	7268	342	113	221	2.8e-18

Description

sp:[LN:YTXJ_BACSU] [AC:P39914] [GN:YTXJ] [OR:BACILLUS SUBTILIS] [DE:(ORF3)]
[SP:P39914] [DB:swissprot] >pir:[LN:S21420] [AC:S21420:F70003:S71003]
[PN:general stress protein homolog ytxJ] [GN:ytxJ] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:g39815] [LN:BSAROAG] [AC:X65945] [GN:orf 2] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis aroA-aroG gene.] [SP:P39914]
[LE:105] [RE:431] [DI:direct] >gp:[GI:e1185849:g2635460] [LN:BSUB0016]
[AC:Z99119:AL009126] [GN:ytxJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
from 2997771to 3213410.] [NT:alternate gene name: csb40; similar to general]
[SP:P39914] [LE:48061] [RE:48387] [DI:complement] >gp:[GI:g2293219]
[LN:AF008220] [AC:AF008220] [PN:YtxJ] [GN:ytxJ] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
[LE:132039] [RE:132365] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_26176693_f2_482	3497	7269	828	275	685	1.9e-67

Description

pir:[LN:A69162] [AC:A69162] [PN:gufA protein homolog MTH473] [GN:MTH473]
[CL:gufA protein] [OR:Methanobacterium thermoautotrophicum] [DB:pir2]
>gp:[GI:g2621542] [LN:AE000831] [AC:AE000831:AE000666] [PN:conserved
protein] [GN:MTH473] [OR:Methanobacterium thermoautotrophicum]
[DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 404817
to 415582(section 37 of 148) of the complete genome.] [NT:Function
Code:14.01 - Unknown, Conserved protein;] [LE:9769] [RE:10548] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_2618827_c1_1042	3498	7270	288	95	75	0.023

Description

sp:[LN:LUXY_VIBFI] [AC:P21578] [GN:LUXY] [OR:VIBRIO FISCHERI] [DE:YELLOW
FLUORESCENT PROTEIN (YFP)] [SP:P21578] [DB:swissprot] >pir:[LN:A36037]
[AC:A36037:A39946] [PN:yellow fluorescent protein:luxY protein] [GN:luxY]
[CL:riboflavin synthase alpha chain] [OR:Vibrio fischeri] [DB:pir2]
>gp:[GI:g155235] [LN:VIBLUXY] [AC:M60852] [PN:yellow fluorescent protein]
[GN:luxY] [OR:Vibrio fischeri] [SR:V.fischeri (strain Y-1) DNA]
[DB:genpept-bct1] [DE:Vibrio fischeri yellow fluorescent protein (luxY)
gene, completecds.] [LE:45] [RE:629] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_26190785_c2_1306	3499	7271	1287	428	1408	4.7e-144

Description

pir:[LN:F70019] [AC:F70019] [PN:Nifs protein homolog homolog yurW] [GN:yurW]
 [CL:nifs protein] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184347:g2635765] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yurW]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
 Nifs protein homolog] [LE:159503] [RE:160723] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_26204837_f1_69	3500	7272	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_26211552_c2_1270	3501	7273	984	327	1034	2.0e-104

Description

pir:[LN:B70032] [AC:B70032] [PN:conserved hypothetical protein yvcL]
 [GN:yvcL] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186163:g2635988]
 [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcL] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins]
 [LE:169083] [RE:170033] [DI:complement] >gp:[GI:e313028:g1945652]
 [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvcL] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).]
 [NT:similar to Y103_MYCGE hypothetical protein mg103] [LE:11638] [RE:12588]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_26259638_f1_134	3502	7274	765	254	176	2.2e-11

Description

pir:[LN:B70798] [AC:B70798] [PN:probable membrane protein] [GN:Rv3737]
[OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e1264597:g2960161]
[LN:MTV025] [AC:AL022121:AL123456] [PN:hypothetical protein Rv3737]
[GN:Rv3737] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1]
[DE:Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.]
[NT:Rv3737, (MTV025.085), len: 529. Probable membrane] [LE:94796] [RE:96385]
[DI:direct] >gp:[GI:e1264597:g2960161] [LN:MTV025] [AC:AL022121:AL123456]
[PN:hypothetical protein Rv3737] [GN:Rv3737] [OR:Mycobacterium tuberculosis]
[DB:genpept] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment
155/162.] [NT:Rv3737, (MTV025.085), len: 529. Probable membrane] [LE:94796]
[RE:96385] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_26359805_f1_11	3503	7275	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_26360663_c3_1530	3504	7276	1308	435	1039	5.9e-105

Description

pir:[LN:A70015] [AC:A70015] [PN:NADH dehydrogenase homolog yumB] [GN:yumB]
[CL:NADH dehydrogenase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184289:g2635707] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yumB]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
NADH dehydrogenase] [LE:102091] [RE:103311] [DI:complement]
>gp:[GI:e311467:g1934829] [LN:BSZ93939] [AC:Z93939] [PN:NADH dehydrogenase]
[GN:yumB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic
DNA fragment from yumA to yulF.] [NT:putative; unknown] [LE:528] [RE:1748]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_26367175_c3_1476	3505	7277	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_26578577_c1_1065	3508	7280	1791	596	2276	1.8e-238

Description

sp:[LN:UVRA_BACSU] [AC:O34863] [GN:UVRA] [OR:BACILLUS SUBTILIS]
[DE:EXCINUCLEASE ABC SUBUNIT A] [SP:O34863] [DB:swissprot] >pir:[LN:F69729]
[AC:F69729] [PN:excinuclease ABC chain A:excision endonuclease ABC,, chain
A:uvrA protein] [GN:uvrA] [CL:excinuclease ABC chain A:ATP-binding cassette
homology] [OR:Bacillus subtilis] [EC:3.1.-.-] [DB:pir2]
>gp:[GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet
light-induced] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 19 of 21): from 3597091to 3809700.]
[SP:O34863] [LE:12034] [RE:14907] [DI:complement] >gp:[GI:g2618842]
[LN:AF017113] [AC:AF017113] [PN:excinuclease ABC subunit A] [GN:uvrA]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304
degree genomic sequence.] [LE:15386] [RE:18259] [DI:direct]
>gp:[GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet
light-induced] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [SP:O34863]
[LE:12034] [RE:14907] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_26594050_c3_1524	3509	7281	243	80	378	6.5e-35

Description

gp:[GI:d1013748:g1405337] [LN:D86240] [AC:D86240] [PN:D-alanyl carrier
protein] [GN:dltC] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(isolate:KAN96) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus gene for
unkown function and dlt operon dltA,dltB, dltC and dltD genes,complete cds.]
[NT:Sequence homologous to the dltC genes of] [LE:5303] [RE:5539]
[DI:direct] >gp:[GI:g4530243] [LN:AF101234] [AC:AF101234] [PN:D-alanine
carrier protein DltC] [GN:dltC] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[DE:Staphylococcus aureus dltABCD operon, complete sequence; andunknown
gene.] [LE:4276] [RE:4512] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_26735877_c3_1508	3510	7282	402	133	446	4.1e-42

Description

pir:[LN:A70021] [AC:A70021] [PN:glycine cleavage system protein H homolog yusH] [GN:yusH] [CL:glycine cleavage system protein H: lipoyl/biotin-binding homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184358:g2635776] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to glycine cleavage system protein H] [LE:168182] [RE:168565] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_26753150_f1_147	3511	7283	336	111	295	4.1e-26

Description

sp:[LN:YKI4_YEAST] [AC:P36078] [GN:YKL084W] [OR:SACCHAROMYCES CEREVISIAE] [SR:,BAKER'S YEAST] [DE:HYPOTHETICAL 13.6 KD PROTEIN IN MDH1-VMA5 INTERGENIC REGION] [SP:P36078] [DB:swissprot] >pir:[LN:S37909] [AC:S37909] [PN:hypothetical protein YKL084w] [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:11L] >gp:[GI:g486123] [LN:SCYKL084W] [AC:Z28084:Y13137] [OR:Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-pln1] [DE:S.cerevisiae chromosome XI reading frame ORF YKL084w.] [NT:ORF YKL084w] [SP:P36078] [LE:382] [RE:732] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_26757807_f2_578	3512	7284	951	316	1619	2.0e-166

Description

gp:[GI:e255529:g1617430] [LN:SEABCTS] [AC:X99127] [PN:lipoprotein] [FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.] [LE:1621] [RE:2550] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_26834387_f1_234	3513	7285	711	236	115	1.2e-06

Description

gp:[GI:g3043880] [LN:LLU95841] [AC:U95841] [PN:transmembrane protein Tmp6] [OR:Lactococcus lactis] [DB:genpept-bct2] [DE:Lactococcus lactis transmembrane protein Tmp6 gene, partial cds.] [NT:identified as a fusion to a signal peptide-less] [LE:<1] [RE:354] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_26839462_c3_1474	3514	7286	1011	336	817	2.0e-81

Description

sp:[LN:YVCK_BACSU] [AC:O06974] [GN:YVCK] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRXB INTERGENIC REGION] [SP:O06974]
 [DB:swissprot] >gp:[GI:e313027:g1945651] [LN:BSZ94043] [AC:Z94043]
 [PN:hypothetical protein] [GN:yvck] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis genomic DNA fragment (88 kb).] [NT:similar to hypothetical
 SYCSLRA] [SP:O06974] [LE:10662] [RE:11615] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_2752262_c3_1426	3515	7287	1014	337	652	6.0e-64

Description

pir:[LN:G69669] [AC:G69669] [PN:choline ABC transporter (ATP-binding
 protein) opuBA] [GN:opuBA] [CL:glycine betaine/proline transport protein
 proV: ATP-binding cassette homology:CBS homology] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1186061:g2635886] [LN:BSUB0018] [AC:Z99121:AL009126]
 [PN:choline ABC transporter (ATP-binding protein)] [GN:opuBA] [FN:high
 affinity transport of choline] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to
 3609060.] [NT:alternate gene name: proV] [LE:61618] [RE:62763]
 [DI:complement] >gp:[GI:g2293447] [LN:AF008930] [AC:AF008930] [PN:ATPase]
 [GN:opuBA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 choline transport system including ATPase(opuBA), transmembrane protein
 (opuBB), choline binding proteinprecursor (opuBC) and transmembrane protein
 (opuBD) genes, completecds; and unknown gene.] [NT:OpuBA; part of choline
 uptake system] [LE:881] [RE:2026] [DI:direct]

666227 6960540

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_275268_c2_1225	3516	7288	1125	374	766	5.0e-76
Description						
sp: [LN:HIS8_BACSU] [AC:P17731:O32008] [GN:HISC:HISH] [OR:BACILLUS SUBTILIS] [EC:2.6.1.9] [DE:PHOSPHATE TRANSAMINASE]] [SP:P17731:O32008] [DB:swissprot] >pir: [LN:A26532] [AC:A26532:G22794:H69640] [PN:histidinol-phosphate transaminase, / tyrosine and phenylalanine aminotransferase hisC:histidinol-phosphate aminotransferase] [GN:hisc:hish] [CL:probable histidinol-phosphate transaminase] [OR:Bacillus subtilis] [EC:2.6.1.9] [DB:pir2] [MP:205 (degrees)] >gp: [GI:g143814] [LN:BACVARGNS] [AC:M80245:M15409] [PN:Hish] [GN:hish] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B.subtilis dbpA, mtr(A,B), gerC(1-3), ndk, cheR, aro(B,E,F,H), trp(A-F), hisH, and tyrA genes, complete cds.] [LE:14250] [RE:15332] [DI:direct] >gp: [GI:e1183707:g2634680] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:tyrosine/phenylalanine aminotransferase] [GN:hisc] [FN:histidine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.6.1.9:2.6.1.5] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541 to 2409220.] [NT:alternate gene name: aroJ; histidinol-phosphate] [SP:P17731] [LE:174116] [RE:175198] [DI:complement]						

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_2917200_f1_277	3517	7289	192	63		
Description						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_2926425_f2_465	3518	7290	960	319	456	3.5e-43
<u>Description</u>						

sp:[LN:BMRU_BACSU] [AC:P39074] [GN:BMRU] [OR:BACILLUS SUBTILIS] [DE:BMRU PROTEIN] [SP:P39074] [DB:swissprot] >pir:[LN:F69595] [AC:F69595]
 [PN:multidrug resistance protein cotranscribed with bmr bmrU] [GN:bmrU]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g409286] [LN:BACBMRURBE]
 [AC:L25604] [GN:bmrU] [FN:unknown, but cotranscribed with bmr] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis bmrU, multidrug efflux transporter (bmr) and itsregulator (bmrR) genes, complete cds, and branched-chain 2-oxo aciddehydrogenase (bfmB) gene, 3' end.] [LE:227] [RE:1120] [DI:direct] >gp:[GI:d1013282:g1303947] [LN:BACJH642] [AC:D84432:D82370] [PN:BmrU] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:225092] [RE:225985] [DI:complement] >gp:[GI:e1185668:g2634834] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:multidrug resistance protein] [GN:bmrU] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P39074] [LE:97634] [RE:98527] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_2929517_c3_1399	3519	7291	126	41		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_29376503_f2_504	3520	7292	246	81		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_29378425_f3_790	3521	7293	132	43		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_29501510_c1_950	3522	7294	1125	374	432	1.2e-40

Description

sp:[LN:TAGB_BACSU] [AC:P27621] [GN:TAGB] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR] [SP:P27621] [DB:swissprot]
 >pir:[LN:C49757] [AC:C49757:C69720] [PN:polyglycerol phosphate techoic acid biosynthesis protein tagB] [GN:tagB] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:g143725] [LN:BACTAGABCD] [AC:M57497] [GN:tagB] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) DNA] [DB:genpept-bct1] [DE:B.subtilis tagA, tagB, tagC and tagD genes, complete cds.] [NT:putative] [LE:1603] [RE:2748] [DI:direct] >gp:[GI:e1184482:g2636102] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagB] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27621] [LE:84143] [RE:85288] [DI:direct] >gp:[GI:e1184482:g2636102] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagB] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27621] [LE:84143] [RE:85288] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_29570877_c3_1414	3523	7295	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_3001313_c2_1262	3524	7296	681	226	154	3.6e-11

Description

pir:[LN:A65001] [AC:A65001] [PN:hypothetical protein b2291] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1788628] [LN:AE000318] [AC:AE000318:U00096] [PN:putative alpha helix protein] [GN:b2291] [FN:phenotype; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 208 of 400 of the completegenome.] [NT:o199] [LE:4988] [RE:5587] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_30198587_f3_629	3525	7297	258	85	306	2.8e-27

Description

pir:[LN:C70024] [AC:C70024] [PN:NifU protein homolog homolog yutI] [GN:yutI] [CL:conserved hypothetical nifU-like protein HP1492] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184301:g2635719] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to NifU protein homolog] [LE:112444] [RE:112779] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_30265692_c3_1521	3526	7298	1050	349	1070	3.1e-108

Description

gp:[GI:g4530240] [LN:AF101234] [AC:AF101234] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus dltABCD operon, complete sequence; and unknown gene.] [NT:Orf1; similar to hydroxyacid dehydrogenases] [LE:51] [RE:1010] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_30272661_f1_265	3527	7299	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_30491275_c1_961	3528	7300	1104	367	391	2.7e-36

Description

pir:[LN:H69867] [AC:H69867] [PN:conserved hypothetical protein ykvI] [GN:ykvI] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184961:g2633742] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins from B. subtilis] [LE:42768] [RE:43811] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_30601588_c3_1356	3529	7301	834	277	561	2.6e-54

Description

sp:[LN:TAGG_BACSU] [AC:P42953] [GN:TAGG] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG] [SP:P42953] [DB:swissprot]
>pir:[LN:S69202] [AC:S69202:H69720] [PN:teichoic acid permease
tagG:integral membrane protein tagG] [GN:tagG] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:g755152] [LN:BSU13832] [AC:U13832] [PN:highly hydrophobic
integral membrane protein] [GN:tagG] [FN:teichoic acid translocation]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly
hydrophobic integral membrane protein(tagG) gene and ATP-binding protein
(tagH) gene, complete cds.] [LE:287] [RE:1114] [DI:direct]
>gp:[GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease]
[GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21):
from 3597091to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement]
>gp:[GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease]
[GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis]
[DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_30661260_c1_1080	3530	7302	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_30745328_c1_1103	3531	7303	606	201	200	4.8e-16

Description

pir:[LN:S56619] [AC:S56619:B65255] [PN:gpmB protein:hypothetical protein
o215b] [GN:gpmB] [CL:phosphoglycerate mutase homology] [OR:Escherichia
coli] [DB:pir2] >gp:[GI:g537235] [LN:ECOUW93] [AC:U14003] [OR:Escherichia
coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from
92.8 to 00.1 minutes.] [NT:Kenn Rudd identifies as gpmB] [LE:324630]
[RE:325277] [DI:direct] >gp:[GI:g1790856] [LN:AE000509] [AC:AE000509:U00096]
[PN:phosphoglyceromutase 2] [GN:gpmB] [FN:enzyme; Energy metabolism, carbon:
Glycolysis] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli
K-12 MG1655 section 399 of 400 of the completegenome.] [LE:8985] [RE:9632]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_31257943_c2_1156	3532	7304	414	137	669	9.5e-66

Description

gp:[GI:g1913907] [LN:SAU91741] [AC:U91741] [PN:TagD] [GN:tagD] [FN:teichoic acid biosynthesis] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus teichoic acid biosynthesis TagB gene, partialcds and TagX and TagD genes, complete cds.] [NT:similar to Bacillus subtilis TagD] [LE:1534] [RE:1932] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_31267503_c2_1168	3533	7305	813	270	784	6.2e-78

Description

pir:[LN:A70001] [AC:A70001] [PN:ABC transporter (ATP-binding protein) homolog ytsC] [GN:ytsC] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185911:g2635522] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:112638] [RE:113399] [DI:complement] >gp:[GI:g2293177] [LN:AF008220] [AC:AF008220] [PN:transporter] [GN:ytsC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:67028] [RE:67789] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_31289687_c1_1051	3534	7306	681	226	132	5.1e-06

Description

gp:[GI:g4894306] [LN:AF065404] [AC:AF065404] [PN:pXO1-90] [OR:Bacillus anthracis] [DB:genpept-bct2] [DE:Bacillus anthracis virulence plasmid PX01, complete sequence.] [LE:106772] [RE:108730] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_31428188_f2_401	3535	7307	222	73		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_31578_c2_1265	3536	7308	537	178	463	6.4e-44

Description

pir:[LN:H70044] [AC:H70044] [PN:O-acetyltransferase homolog yvoF] [GN:yvoF]
] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186184:g2636009] [LN:BSUB0018]
 [AC:Z99121:AL009126] [GN:yvoF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
 from 3399551to 3609060.] [NT:similar to O-acetyltransferase] [LE:190798]
 [RE:191316] [DI:complement] >gp:[GI:g2618861] [LN:AF017113] [AC:AF017113]
 [PN:putative acetyltransferase] [GN:yvoF] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.]
 [LE:36517] [RE:37035] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_31803377_f3_884	3537	7309	612	203		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_31876563_c1_1124	3538	7310	1239	412	1924	9.7e-199

Description

gp:[GI:d1013747:g1405336] [LN:D86240] [AC:D86240] [PN:hypothetical membrane
 transporter] [GN:dltB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 (isolate:KAN96) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus gene for
 unkown function and dlt operon dltA,dltB, dltC and dltD genes,complete cds.]
 [NT:Sequence homologous to the dltB genes of] [LE:4071] [RE:5285]
 [DI:direct] >gp:[GI:g4530242] [LN:AF101234] [AC:AF101234] [PN:putative
 membrane protein DltB] [GN:dltB] [FN:involved in D-alanine transfer into
 teichoic] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
 aureus dltABCD operon, complete sequence; andunknown gene.] [LE:3044]
 [RE:4258] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_32062553_c1_943	3539	7311	468	155	354	2.3e-32

Description

pir:[LN:S61393] [AC:S61393] [PN:hypothetical protein 2] [OR:Bacillus sp.]
 [SR:strain C-125, , strain C-125] [SR:strain C-125,] [DB:pir2]
 >gp:[GI:d1007182:g854656] [LN:BACAPS] [AC:D31823] [PN:ORF2] [OR:Bacillus
 sp.] [SR:Bacillus sp. (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus sp.
 Na+/H+ antiporter system responsible genes.] [NT:Na+/H+ antiporter system
 responsible gene] [LE:2669] [RE:3109] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_32070827_f3_789	3540	7312	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_32212902_c2_1135	3541	7313	1035	344	468	1.9e-44

Description

pir:[LN:F70046] [AC:F70046] [PN:iron permease homolog yvrB] [GN:yvrB]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1249808:g2832812] [LN:BS43KBDNA]
[AC:AJ223978] [PN:putative hemin permease, YvrB] [GN:yvrB] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from
yvsA to yvqA.] [LE:24699] [RE:25760] [DI:direct] >gp:[GI:e1184396:g2635814]
[LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvrB] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
17 of 21): from 3197001to 3414420.] [NT:similar to iron permease]
[LE:204527] [RE:205588] [DI:complement] >gp:[GI:e1186005:g2635830]
[LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvrB] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
18 of 21): from 3399551to 3609060.] [NT:similar to iron permease] [LE:1977]
[RE:3038] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_32225012_f1_54	3542	7314	498	165	276	4.2e-24

Description

pir:[LN:F69870] [AC:F69870] [PN:general stress protein homolog ykzA]
[GN:ykzA] [CL:hypothetical protein yklA] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1181516:g2632036] [LN:BSAJ2571] [AC:AJ002571] [PN:YknA] [GN:yknA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
168 56 kb DNA fragment between xlyA and ykoR.] [NT:homologous to OsmC from
Escherichia coli] [LE:34145] [RE:34555] [DI:direct]
>gp:[GI:e1183336:g2633670] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykzA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 7 of 21): from 1194391to 1411140.] [NT:alternate
gene name: yzzE; similar to general] [LE:187094] [RE:187504] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_32475037_f3_651	3543	7315	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_32611068_c1_927	3544	7316	1674	557	1694	2.3e-174

Description

sp:[LN:SYR_BACSU] [AC:P46906] [GN:ARGS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.19] [DE:ARGINYL-TRNA SYNTHETASE, (ARGININE--TRNA LIGASE) (ARGRS)] [SP:P46906] [DB:swissprot] >pir:[LN:E69589] [AC:E69589:S60082] [PN:arginine--trna ligase, argS:arginyl-trna synthetase] [GN:argS] [CL:Bacillus arginine--trna ligase] [OR:Bacillus subtilis] [EC:6.1.1.19] [DB:pir2] >gp:[GI:e1186234:g2636270] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:arginyl-trna synthetase] [GN:argS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.19] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [SP:P46906] [LE:34303] [RE:35973] [DI:complement] >gp:[GI:e324388:g2224756] [LN:BSZ97024] [AC:Z97024] [PN:arginyl trna synthetase] [GN:argS] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ywiA, sbo, ywiB, argS and narK genes.] [SP:P46906] [LE:1680] [RE:3350] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_33210952_f2_370	3545	7317	234	77	93	0.0025

Description

gp:[GI:g3859891] [LN:AF072678] [AC:AF072678] [PN:alpha-actinin] [GN:AACTI] [OR:Trichomonas vaginalis] [DB:genpept-inv2] [DE:Trichomonas vaginalis alpha-actinin (AACTI) mRNA, complete cds.] [NT:actin binding protein] [LE:247] [RE:3042] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_33239001_f2_356	3546	7318	276	91		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_33304063_f1_151	3547	7319	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_33414143_c3_1395	3548	7320	1710	569	619	1.9e-60

Description

gp:[GI:g2773332] [LN:AF040718] [AC:AF040718] [PN:ABC transporter CydC]
 [GN:cydC] [OR:Shigella flexneri] [DB:genpept-bct2] [DE:Shigella flexneri ABC
 transporter CydC (cydC) gene, complete cds.] [NT:similar to E. coli CydC]
 [LE:1648] [RE:3369] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_33628441_f3_645	3549	7321	255	84		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_33645967_f1_18	3550	7322	282	93	73	0.019

Description

gp:[GI:g2444074] [LN:CPU88070] [AC:U88070] [GN:scc1] [FN:putative chaperone
 of type III secretory] [OR:Chlamydophila caviae] [DB:genpept-bct2]
 [DE:Chlamydophila caviae cds1, cds2, copN and scc1 genes, complete cds.]
 [NT:similar to SycE of Yersinia] [LE:4766] [RE:5206] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34069680_c1_1125	3551	7323	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34160625_c3_1368	3552	7324	438	145		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34173262_c3_1497	3553	7325	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34173385_c1_975	3554	7326	621	206	151	7.4e-11

Description

pir:[LN:E71040] [AC:E71040] [PN:hypothetical protein PH1613] [GN:PH1613]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031668:g3258042]
 [LN:AP000006]
 [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514]
 [PN:166aa long hypothetical protein] [GN:PH1613] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi]
 [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000
 nt. position(6/7).] [LE:263709] [RE:264209] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34173750_c3_1485	3555	7327	480	159		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34176550_f1_24	3556	7328	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34189817_c1_945	3557	7329	2052	683	888	5.9e-89

Description

pir:[LN:E70040] [AC:E70040] [PN:conserved hypothetical protein yvgP]
 [GN:yvgP] [CL:hypothetical protein yvgP] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1186030:g2635855] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgP]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to
 hypothetical proteins] [LE:27843] [RE:29855] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34242162_c3_1511	3558	7330	489	162	529	6.5e-51

Description

pir:[LN:E70019] [AC:E70019] [PN:NifU protein homolog homolog yurV] [GN:yurV]
] [CL:Yeast nitrogen fixation protein:nitrogen fixation protein homology]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184346:g2635764] [LN:BSUB0017]
 [AC:Z99120:AL009126] [GN:yurV] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
 from 3197001to 3414420.] [NT:similar to NifU protein homolog] [LE:159070]
 [RE:159513] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34251887_c2_1322	3559	7331	1266	421	1649	1.3e-169

Description

gp:[GI:g4530244] [LN:AF101234] [AC:AF101234] [PN:putative exoprotein DltD]
 [GN:dltD] [FN:involved in D-alanine transfer into teichoic]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 dltABCD operon, complete sequence; and unknown gene.] [LE:4509] [RE:5684]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34254581_c1_954	3560	7332	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34261088_c3_1387	3561	7333	312	103	75	0.018

Description

gp:[GI:g488925] [LN:A13473] [AC:A13473] [PN:41kd antigen] [OR:Plasmodium
 falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-pat]
 [DE:P.falciparum gene for 41kd antigen, clone 41-14.] [LE:<1] [RE:>532]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34562762_c3_1336	3562	7334	750	249	230	3.2e-19

Description

pir:[LN:D71157] [AC:D71157] [PN:hypothetical protein PH0459] [GN:PH0459]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030488:g3256862]
 [LN:AP000002]
 [AC:AP000002:AB009475:AB009476:AB009477:AB009478:AB009479:AB009480]
 [PN:232aa long hypothetical protein] [GN:PH0459] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 287001-544000 nt. position(2/7).] [LE:132975]
 [RE:133673] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34571000_f1_163	3563	7335	537	178	393	1.7e-35

Description

sp:[LN:ADH2_ENTHI] [AC:Q24803:Q27649] [GN:ADH2] [OR:ENTAMOEBA HISTOLYTICA]
 [EC:1.1.1.1:1.2.1.10] [DE:DEHYDROGENASE, (ACDH)] [SP:Q24803:Q27649]
 [DB:swissprot] >gp:[GI:g488430] [LN:EHU04863] [AC:U04863] [PN:alcohol
 dehydrogenase 2] [OR:Entamoeba histolytica] [DB:genpept-inv1] [DE:Entamoeba
 histolytica HM1:IMSS alcohol dehydrogenase 2 (EhADH2)mRNA, complete cds.]
 [NT:The derived amino acid sequence of EhADH2 is] [LE:3] [RE:2615]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34589027_c2_1197	3564	7336	315	104	98	0.00023

Description

sp:[LN:Y420_METJA] [AC:Q57863] [GN:MJ0420] [OR:METHANOCOCCUS JANNASCHII]
 [DE:HYPOTHETICAL PROTEIN MJ0420] [SP:Q57863] [DB:swissprot] >pir:[LN:D64352]
 [AC:D64352] [PN:hypothetical protein MJ0420] [OR:Methanococcus jannaschii]
 [DB:pir2] [MP:FOR378394-379536] >gp:[GI:g1591123] [LN:U67494]
 [AC:U67494:L77117] [PN:O-antigen polymerase isolog] [GN:MJ0420]
 [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii
 section 36 of 150 of the complete genome.] [NT:similar to GB:M60066
 SP:P26479 PID:154343 percent] [LE:1855] [RE:2997] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_34612887_f2_512	3565	7337	465	154	260	2.1e-22

Description

pir:[LN:E69857] [AC:E69857] [PN:conserved hypothetical protein ykmA] [GN:ykMA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181515:g2632035] [LN:BSAJ2571] [AC:AJ002571] [PN:YkMA] [GN:ykMA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [LE:33559] [RE:34002] [DI:complement] >gp:[GI:e1183335:g2633669] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykMA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to hypothetical proteins] [LE:186508] [RE:186951] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_34627136_f3_681	3566	7338	306	101	73	0.014

Description

pir:[LN:S36690] [AC:S36690] [PN:hypothetical protein] [OR:Autographa californica nuclear polyhedrosis virus:AcMNPV] [DB:pir2] >gp:[GI:g296321] [LN:ACNPVDNA] [AC:X71415] [GN:ORF 339] [OR:Autographa californica nucleopolyhedrovirus] [DB:genpept-vrl] [DE:Autographa californica nuclear polyhedrosis virus DNA.] [SP:Q06669] [LE:<1] [RE:339] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_34641875_c3_1406	3567	7339	939	312	704	1.9e-69

Description

pir:[LN:A69627] [AC:A69627] [PN:fructose 1-phosphate kinase fruB] [GN:fruB] [CL:6-phosphofructokinase 2] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185029:g2633810] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:fructose-1-phosphate kinase] [GN:fruB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.56] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [LE:112945] [RE:113856] [DI:direct] >gp:[GI:g3282124] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:fructose-1-phosphate kinase] [GN:fruB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to L. lactis tagatose-6-phosphate kinase,] [LE:13433] [RE:14344] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34642567_c1_1089	3568	7340	2406	801	2175	1.0e-228

Description

pir:[LN:G70027] [AC:G70027] [PN:conserved hypothetical protein yvaJ]
 [GN:yvaJ] [CL:virulence-associated protein vacB homolog] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e1186049:g2635874] [LN:BSUB0018]
 [AC:Z99121:AL009126] [GN:yvaJ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
 from 3399551to 3609060.] [NT:similar to hypothetical proteins] [LE:51375]
 [RE:53714] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_34645311_f3_867	3569	7341	525	174	186	1.4e-14

Description

gp:[GI:g4981094] [LN:AE001732] [AC:AE001732:AE000512] [PN:conserved
 hypothetical protein] [GN:TM0577] [OR:Thermotoga maritima] [DB:genpept-bct2]
 [DE:Thermotoga maritima section 44 of 136 of the complete genome.]
 [NT:similar to SP:P46854 PID:606376 GB:U00096] [LE:9820] [RE:10359]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_3518_f2_375	3570	7342	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_35422880_c2_1228	3571	7343	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_35444127_f2_443	3572	7344	663	220	514	2.5e-49

Description

sp:[LN:YVYE_BACSU] [AC:P32437:P96500] [GN:YVYE:YVHK] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 24.8 KD PROTEIN IN DEGS-TAGO INTERGENIC REGION]
[SP:P32437:P96500] [DB:swissprot] >pir:[LN:A70049] [AC:A70049:A30191]
[PN:conserved hypothetical protein yvyE] [GN:yvyE] [CL:hypothetical protein
HI0722] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184457:g2636077]
[LN:BSUB0019] [AC:Z99122:AL009126] [GN:yvyE] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
19 of 21): from 3597091to 3809700.] [NT:alternate gene name: yvhK; similar
to hypothetical] [SP:P32437] [LE:48723] [RE:49376] [DI:direct]
>gp:[GI:g1762328] [LN:BSU56901] [AC:U56901] [PN:Ycr59c/YigZ homolog]
[GN:yvhK] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
putative transcriptional regulator (yvhJ),Ycr59c/YigZ homolog (yvhK),
histidine kinase (degS),transcriptionalregulator of degradation enzyme
(degU), (degV), (comFA), (comFB), (comFC), flagellar protein (yviB), negative
regulator of flagellin(flgM), flagellar protein (yviC), flagellar-hook
associated protein1 (flgK), flagellar-hook associated protein 3 (flgL),
(yviE),transmembrane protein (yviF), (csrA), flagellin (hag),
flagellarprotein (yviH), flagellar hook-associated protein 2
(fliD),flagellar protein (fliS), flagellar protein (fliT), sigma-54modulator
homolog (yviI), and (secA) genes, complete cds.] [LE:1217] [RE:1870]
[DI:complement] >gp:[GI:e1184457:g2636077] [LN:BSUB0019]
[AC:Z99122:AL009126] [GN:yvyE] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:alternate gene name: yvhK; similar to hypothetical]
[SP:P32437] [LE:48723] [RE:49376] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_35945277_c3_1463	3573	7345	1065	354	1275	5.8e-130

Description

sp: [LN:RF2_BACSU] [AC:P28367:O34444] [GN:PRFB] [OR:BACILLUS SUBTILIS]
[DE:PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)] [SP:P28367:O34444] [DB:swissprot]
>pir: [LN:JN0146] [AC:H69681:JN0146] [PN:translation releasing factor
RF-2:peptide chain release factor 2:prfB] [GN:prfB] [CL:translation
releasing factor] [OR:Bacillus subtilis] [DB:pir1]
>gp: [GI:e1184435:g2636055] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:peptide
chain release factor 2] [GN:prfB] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
3809700.] [SP:P28367] [LE:29109:30139] [RE:30137:30210] [DI:complementJoin]
>gp: [GI:g2331287] [LN:AF013188] [AC:AF013188] [PN:release factor 2]
[GN:prfB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
release factor 2 (prfB) gene, complete cds.] [NT:orf3; naturally occurring
frame-shift] [LE:75:148] [RE:146:1176] [DI:directJoin] >gp: [GI:g2618874]
[LN:AF017113] [AC:AF017113] [PN:putative peptide chain release factor RF-2]
[GN:prfB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
300-304 degree genomic sequence.] [LE:83:156] [RE:154:1184] [DI:directJoin]
>gp: [GI:e1184435:g2636055] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:peptide
chain release factor 2] [GN:prfB] [OR:Bacillus subtilis] [DB:genpept]
[DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
3809700.] [SP:P28367] [LE:29109:30139] [RE:30137:30210] [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_35988961_f2_376	3574	7346	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_36131311_c3_1455	3575	7347	696	231	194	2.1e-15
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Description

gp: [GI:g451867] [LN:BACFLGMK] [AC:L14437] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain W168) (library: lambda gtWES library)
[DB:genpept-bct1] [DE:Bacillus subtilis (clones pDM116 and pDM113) flagellin
synthesisregulatory protein (flgM) and flagellar hook-filament
junctionprotein (flgK) genes and orf139, orf160, orfX, complete cds's.]
[NT:in Z18629, ORFX is called comForf3; ORFX; putative] [LE:<1] [RE:754]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_36133385_c3_1377	3576	7348	681	226	203	2.3e-16

Description

pir:[LN:G69798] [AC:G69798] [PN:hypothetical protein yetJ] [GN:yetJ]
[CL:hypothetical protein yetJ] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182699:g2633033] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yetJ]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 4 of 21): from 600701 to813890.] [LE:186800]
[RE:187444] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_36229676_c1_936	3577	7349	795	264	238	4.5e-20

Description

gp:[GI:g3172115] [LN:ACCPAOP]
[AC:L05770:U04359:M33798:U20284:U11554:L13114:L03407] [PN:beta-ketoadipate
enol-lactone hydrolase] [GN:pcaD] [OR:Acinetobacter sp. ADP1]
[DB:genpept-bct2] [EC:3.1.1.24] [DE:Acinetobacter sp. ADP1 pca-qui-pob
supraoperonic cluster, completesequence.] [NT:ELH] [LE:6843] [RE:7643]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_36230252_c1_1000	3578	7350	777	258	480	1.0e-45

Description

pir:[LN:B69627] [AC:B69627] [PN:transcription repressor of fructose operon
fruR] [GN:fruR] [CL:regulatory protein gutR] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1185028:g2633809] [LN:BSUB0008] [AC:Z99111:AL009126]
[PN:transcriptional regulator (DeoR family)] [GN:fruR] [FN:negative
regulation of the fructose operon] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to
1603020.] [LE:112193] [RE:112948] [DI:direct] >gp:[GI:g3282123]
[LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:FruR] [GN:fruR] [OR:Bacillus
subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.]
[NT:similar to L. lactis lactose PTS system repressor,] [LE:12681]
[RE:13436] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_36367302_c3_1330	3579	7351	564	187	122	2.7e-06

Description

sp:[LN:Y359_METJA] [AC:Q57805] [GN:MJ0359] [OR:METHANOCOCCUS JANNASCHII]
[DE:HYPOTHETICAL PROTEIN MJ0359] [SP:Q57805] [DB:swissprot] >pir:[LN:G64344]
[AC:G64344] [PN:hypothetical protein MJ0359] [OR:Methanococcus jannaschii]
[DB:pir2] [MP:REV327449-326805] >gp:[GI:g1591068] [LN:U67489]
[AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0359]
[GN:MJ0359] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
[DE:Methanococcus jannaschii section 31 of 150 of the complete genome.]
[NT:hypothetical protein; identified by GeneMark;] [LE:2497] [RE:3141]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_36563_c2_1302	3580	7352	1074	357	908	4.5e-91

Description

pir:[LN:D70020] [AC:D70020] [PN:ABC transporter (ATP-binding protein)
homolog yusC] [GN:yusC] [CL:ATP-binding cassette homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1184353:g2635771] [LN:BSUB0017]
[AC:Z99120:AL009126] [GN:yusC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
from 3197001to 3414420.] [NT:similar to ABC transporter (ATP-binding
protein)] [LE:165325] [RE:166350] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_36601562_c3_1403	3581	7353	1182	393	1669	1.0e-171

Description

sp:[LN:NORA_STAAU] [AC:P21191] [GN:NORA] [OR:STAPHYLOCOCCUS AUREUS]
[DE:QUINOLONE RESISTANCE NORA PROTEIN] [SP:P21191] [DB:swissprot]
>pir:[LN:A37838] [AC:A37838] [PN:norA protein] [OR:Staphylococcus aureus]
[DB:pir2] >gp:[GI:d1014850:g216975] [LN:STANORA] [AC:D90119] [PN:ORF for
norA] [GN:norA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain
TK2566) genomic DNA] [DB:genpept-bct1] [DE:S. aureus norA gene.] [LE:478]
[RE:1644] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_37927_f1_282	3582	7354	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_391527_f3_880	3583	7355	930	309	700	4.9e-69

Description

sp:[LN:TAGH_BACSU] [AC:P42954] [GN:TAGH] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID TRANSLOCATION ATP-BINDING PROTEIN TAGH] [SP:P42954] [DB:swissprot]
 >pir:[LN:S69203] [AC:S69203:A69721] [PN:teichoic acid translocation ATP-binding protein tagH] [GN:tagH] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g755153] [LN:BSU13832] [AC:U13832] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly hydrophobic integral membrane protein(tagG) gene and ATP-binding protein (tagH) gene, complete cds.] [LE:1134] [RE:2717] [DI:direct]
 >gp:[GI:e1184476:g2636096] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P42954] [LE:75534] [RE:77117] [DI:complement] >gp:[GI:e1184476:g2636096] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P42954] [LE:75534] [RE:77117] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_3922550_f1_67	3584	7356	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_3928762_f2_369	3585	7357	1368	455	839	9.2e-84

Description

pir:[LN:B70007] [AC:B70007] [PN:Na+-transporting ATP synthase homolog yubG] [GN:yubG] [CL:Na+-ATP synthase chain J] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1185983:g2635594] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:yubG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to Na+-transporting ATP synthase] [LE:190389] [RE:191726] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_3939218_c1_922	3586	7358	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_3942263_c3_1381	3587	7359	726	241	913	1.3e-91

Description

pir:[LN:C69793] [AC:C69793] [PN:conserved hypothetical protein yeeI]
 [GN:yeeI] [CL:hypothetical protein MG332] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182664:g2632998] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yeeI]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to
 hypothetical proteins] [LE:151216] [RE:151938] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_3944001_c1_1130	3588	7360	1524	507	684	2.4e-67

Description

pir:[LN:F70012] [AC:F70012] [PN:leucyl aminopeptidase homolog yuiE]
 [GN:yuiE] [CL:cytosol aminopeptidase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184284:g2635702] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuiE]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
 leucyl aminopeptidase] [LE:98474] [RE:99976] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_3948587_f2_340	3589	7361	873	290	378	6.5e-35

Description

gp:[GI:g4980658] [LN:AE001701] [AC:AE001701:AE000512] [PN:conserved
 hypothetical protein] [GN:TM0164] [OR:Thermotoga maritima] [DB:genpept-bct2]
 [DE:Thermotoga maritima section 13 of 136 of the complete genome.]
 [NT:similar to GB:AE000666 percent identity: 61.11;] [LE:9393] [RE:10187]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_3953452_c2_1201	3590	7362	507	168	328	1.3e-29

Description

pir:[LN:D69849] [AC:D69849] [PN:transcription regulation homolog yjdI]
 [GN:yjdI] [CL:conserved hypothetical protein HI1434] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1183226:g2633560] [LN:BSUB0007] [AC:Z99110:AL009126]
 [GN:yjdI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 7 of 21): from 1194391to 1411140.]
 [NT:similar to transcription regulation] [LE:82766] [RE:83245] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_3955067_c2_1278	3591	7363	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_3959377_f3_886	3592	7364	126	41	149	1.7e-10

Description

gp:[GI:e255528:g1617429] [LN:SEABCTS] [AC:X99127] [PN:membrane protein]
[FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis]
[DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.]
[LE:878] [RE:1624] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_3962915_f2_507	3593	7365	627	208	139	1.1e-08

Description

pir:[LN:C71375] [AC:C71375] [PN:conserved hypothetical integral membrane
protein TP0033] [GN:TP0033] [OR:Treponema pallidum subsp. pallidum] [SR:,
syphilis spirochete] [DB:pir2] >gp:[GI:g3322288] [LN:AE001188]
[AC:AE001188:AE000520] [PN:conserved hypothetical integral membrane]
[GN:TP0033] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum
section 4 of 87 of the complete genome.] [NT:similar to PID:1001613
PID:1001643 percent] [LE:7016] [RE:7627] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_39818_f2_530	3594	7366	240	79	234	1.2e-19

Description

gp:[GI:g1575061] [LN:SAU57060] [AC:U57060] [PN:ScdA] [GN:scdA]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus scdA
gene, complete cds.] [NT:S. aureus cells containing a scdA disruption have]
[LE:361] [RE:1035] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_3994027_f1_193	3595	7367	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4023518_f2_400	3596	7368	909	302	579	3.3e-56

Description

pir:[LN:G69800] [AC:G69800] [PN:cell-division inhibitor homolog yfhF]
 [GN:yfhF] [CL:cell division inhibitor yfhF] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1182841:g2633175] [LN:BSUB0005] [AC:Z99108:AL009126]
 [GN:yfhF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 5 of 21): from 802821 to1011250.]
 [NT:similar to cell-division inhibitor] [LE:121320] [RE:122231]
 [DI:complement] >gp:[GI:d1025388:g2804536] [LN:D85082] [AC:D85082] [PN:YfhF]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.]
 [LE:14211] [RE:15122] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4036093_c3_1384	3597	7369	864	287	461	1.0e-43

Description

pir:[LN:B69866] [AC:B69866] [PN:transcription regulator LysR family homolog
 ykuM] [GN:ykuM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181918:g2632234]
 [LN:BS16829KB] [AC:AJ222587] [PN:YkuM protein] [GN:ykuM] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 29kB DNA fragment from
 ykwC gene to cse15 gene.] [NT:homologous to LysR type transcriptional
 regulators] [LE:20403] [RE:21284] [DI:direct] >gp:[GI:e1185004:g2633785]
 [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykuM] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8
 of 21): from 1394791to 1603020.] [NT:similar to transcriptional regulator
 (LysR family)] [LE:90659] [RE:91540] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4072006_f3_845	3598	7370	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4095055_f2_463	3599	7371	894	297	512	4.1e-49

Description

pir:[LN:B71256] [AC:B71256] [PN:conserved hypothetical integral membrane protein TP0986] [GN:TP0986] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2] >gp:[GI:g3323311] [LN:AE001266] [AC:AE001266:AE000520] [PN:conserved hypothetical integral membrane] [GN:TP0986] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum section 82 of 87 of the complete genome.] [NT:similar to GB:AE000511 PID:2314395 percent] [LE:1967] [RE:2851] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4096093_c3_1496	3600	7372	354	117	155	2.8e-11

Description

pir:[LN:B42573] [AC:B42573] [PN:urf120] [OR:Paracoccus denitrificans] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4100093_c3_1419	3601	7373	1161	386	489	1.1e-46

Description

pir:[LN:E64556] [AC:E64556] [PN:para-aminobenzoate synthetase] [OR:Helicobacter pylori] [DB:pir2] >gp:[GI:g2313385] [LN:AE000547] [AC:AE000547:AE000511] [PN:para-aminobenzoate synthetase (pabB)] [GN:HP0293] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 25 of 134 of the complete genome.] [NT:similar to GB:K02673 SP:P05041 GB:U07748 GB:U07749] [LE:20379] [RE:22058] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4101643_c2_1314	3602	7374	399	132	304	4.5e-27

Description

pir:[LN:F70023] [AC:F70023] [PN:hypothetical protein yutD] [GN:yutD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184310:g2635728] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:121344] [RE:121652] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4103393_c2_1215	3603	7375	597	198	436	4.7e-41

Description

sp:[LN:PABA_SALTY] [AC:P06193] [GN:PABA] [OR:SALMONELLA TYPHIMURIUM]
[EC:4.1.3.-] [DE:(EC 4.1.3.-) (ADC SYNTHASE)] [SP:P06193] [DB:swissprot]
>pir:[LN:S09636] [AC:S09636] [PN:pabA protein] [GN:pabA] [CL:glutamine
amidotransferase:trpG homology] [OR:Salmonella typhimurium] [DB:pir2]
>gp:[GI:g47816] [LN:STPABA] [AC:X02603] [OR:Salmonella typhimurium]
[DB:genpept-bct1] [DE:Salmonella typhimurium pabA gene for
para-aminobenzoate synthaseglutamine amidotransferase.] [NT:pabA gene
product (aa 1-187)] [SP:P06193] [LE:1] [RE:564] [DI:direct] >gp:[GI:g154228]
[LN:STYPABAA] [AC:M32355] [OR:Salmonella typhimurium] [SR:S.typhimurium DNA,
clone pSZD3] [DB:genpept-bct1] [DE:S.typhimurium glutamine amidotransferase
subunit ofpara-aminobenzoate synthase (pabA) and pot. cell division
protein] [GN:glutamine amidotransferase] [LE:970]
[RE:1533] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4110888_c3_1380	3604	7376	405	134	93	0.00010

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory
regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis]
[DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory
regulator A homolog (sarA) gene, complete cds.] [LE:887] [RE:1261]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4111691_c1_1018	3605	7377	744	247	351	1.5e-31

Description

sp:[LN:YCSJ_BACSU] [AC:P42967] [GN:YCSJ] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 63.8 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION] [SP:P42967]
[DB:swissprot] >pir:[LN:G69765] [AC:G69765:I39898] [PN:allophanate
hydrolase homolog ycsJ:probable urea amidolyase] [GN:ycsJ] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:d1007939:g790943] [LN:BAC39R] [AC:D38161]
[PN:urea amidolyase] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168TrpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome around
39 degrees region encoding 17 ORFs,complete cds.] [LE:10358] [RE:12094]
[DI:direct] >gp:[GI:e1182375:g2632709] [LN:BSUB0003] [AC:Z99106:AL009126]
[GN:ycsJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 3 of 21): from 402751 to611850.]
[NT:similar to allophanate hydrolase] [SP:P42967] [LE:56667] [RE:58403]
[DI:direct] >gp:[GI:d1009674:g1805477] [LN:D50453] [AC:D50453]
[PN:homologues to hypothetical protein HI1731 of H.] [GN:ycsJ] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa
region, complete cds.] [LE:139065] [RE:140801] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4195817_c1_955	3606	7378	1743	580	2597	4.7e-270

Description

gp:[GI:e264711:g1262136] [LN:SAPBP4GEN] [AC:X91786] [PN:ATP-binding cassette
transporter A] [GN:abcA] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:S.aureus abcA, pbp4, and tagD genes.] [LE:311] [RE:2038] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_42167_c1_959	3607	7379	834	277	1083	1.3e-109

Description

gp:[GI:g4928292] [LN:AF132117] [AC:AF132117] [PN:FhuA] [GN:fhuA]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
ferrichrome uptake operon, complete sequenceand unknown genes.] [NT:ATP
binding protein.] [LE:2780] [RE:3514] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_422162_f3_795	3608	7380	456	151	439	2.2e-41

Description

pir:[LN:B69868] [AC:B69868] [PN:6-pyruvoyl tetrahydrobiopterin synthase homolog ykvK] [GN:ykvK] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184963:g2633744] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to 6-pyruvoyl tetrahydrobiopterin synthase] [LE:44776] [RE:45225] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_422800_f3_903	3609	7381	447	148	627	2.7e-61

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_425927_f1_232	3610	7382	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_429675_f2_558	3611	7383	216	71		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4330390_c3_1517	3612	7384	876	291	787	3.0e-78

Description

pir:[LN:A70016] [AC:A70016] [PN:hypothetical protein yunF] [GN:yunF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184318:g2635736] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yunF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:127975] [RE:128829] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4351465_c2_1159	3613	7385	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4461693_f2_596	3614	7386	240	79		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4487588_f3_797	3615	7387	609	202	81	0.00094
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Description

pir:[LN:B69478] [AC:B69478] [PN:NADH dehydrogenase (ubiquinone),, 43.2 kDa subunit homolog] [OR:Archaeoglobus fulgidus] [EC:1.6.5.3] [DB:pir2]
>gp:[GI:g2648717] [LN:AE000976] [AC:AE000976:AE000782] [PN:F420H2:quinone oxidoreductase, 43.2 kDa subunit,] [GN:AF1827] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 131 of 172 of the complete genome.] [NT:similar to PID:882405 SP:P50973 percent identity:] [LE:4241] [RE:5455] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4501250_c1_1097	3616	7388	1080	359	871	3.7e-87
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Description

gp:[GI:d1020364:g1944409] [LN:D87026] [AC:D87026:D28136] [PN:membrane protein] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (strain:TRBE14) DNA] [DB:genpept-bct1] [DE:Bacillus stearothermophilus glycogen operon genes, complete cds.] [NT:The ORF is similar to the Alkaligenes eutrophus] [LE:144] [RE:1097] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4511550_c2_1247	3617	7389	1278	425	318	1.5e-28
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Description

sp:[LN:YHAD_ECOLI] [AC:P23524] [GN:YHAD] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3)]
[SP:P23524] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4535652_f1_255	3618	7390	225	74		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4539143_c1_1066	3619	7391	942	313	970	1.2e-97
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Description

sp:[LN:HPRK_BACSU] [AC:O34483] [GN:PTSK] [OR:BACILLUS SUBTILIS] [EC:2.7.1.-]
[DE:HPR(SER) KINASE,] [SP:O34483] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4578956_f1_101	3620	7392	297	98	79	0.021
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Description

gp:[GI:e1350598:g3881046] [LN:CEY51A2D] [AC:AL021497] [GN:Y51A2D.12]
[OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans
cosmid Y51A2D, complete sequence.] [LE:83074:83534:84872]
[RE:83208:83768:84978] [DI:complementJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503001001_4687843_c2_1324	3621	7393	330	109	242	1.7e-20
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Description

pir:[LN:C70026] [AC:C70026] [PN:hypothetical protein yuzD] [GN:yuzD]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184300:g2635718] [LN:BSUB0017]
[AC:Z99120:AL009126] [GN:yuzD] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
from 3197001to 3414420.] [LE:112018] [RE:112344] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_4689077_c2_1271	3622	7394	333	110	466	3.1e-44

Description

sp:[LN:CLPP_BACSU] [AC:P80244:O08433] [GN:CLPP] [OR:BACILLUS SUBTILIS]
[EC:3.4.21.92] [DE:(ENDOPEPTIDASE CLP) (CASEINOLYTIC PROTEASE) (PROTEASE
TI)] [SP:P80244:O08433] [DB:swissprot] >pir:[LN:B69601] [AC:B69601:A47683]
[PN:ATP-dependent clp proteinase, chain P:stress protein G7] [GN:clpP]
[CL:ATP-dependent Clp proteinase chain P] [OR:Bacillus subtilis]
[EC:3.4.21.-] [DB:pir2] >gp:[GI:e1186142:g2635967] [LN:BSUB0018]
[AC:Z99121:AL009126] [PN:ATP-dependent Clp protease proteolytic subunit]
[GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.4.21.92]
[DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to
3609060.] [NT:alternate gene name: yvdN] [SP:P80244] [LE:145744] [RE:146337]
[DI:direct] >gp:[GI:e313044:g1945673] [LN:BSZ94043] [AC:Z94043]
[PN:hypothetical protein] [GN:yvdN] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis genomic DNA fragment (88 kb).] [NT:similar to CLPP_ECOLI
ATP-dependent clp protease] [SP:P80244] [LE:35334] [RE:35927]
[DI:complement] >gp:[GI:g2668494] [LN:BSU59754] [AC:U59754] [PN:ClpP]
[GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis Clp
protease proteolytic component (clpP) gene,complete cds.] [NT:proteolytic
component of Clp protease] [LE:140] [RE:733] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_4689130_f2_614	3623	7395	306	101	81	0.029

Description

pir:[LN:A58932] [AC:A58932] [PN:cytochrome C-type biogenesis protein CCMF]
[GN:yejR:ccmF] [OR:mitochondrion Cyanidioschyzon merolae] [DB:pir2]
>gp:[GI:d1037513:g4115789] [LN:D89861] [AC:D89861] [PN:cytochrome C-type
biogenesis protein CCMF] [GN:yejR or ccmF] [OR:Mitochondrion Cyanidioschyzon
merolae] [SR:Cyanidioschyzon merolae (strain:10D) mitochondrion DNA]
[DB:genpept-pln1] [DE:Cyanidioschyzon merolae mitochondrial DNA, complete
sequence.] [LE:16296] [RE:18158] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_4695293_c3_1487	3624	7396	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4703180_c1_1041	3625	7397	453	150	541	3.5e-52

Description

gp:[GI:e1393149:g4490608] [LN:SAU133495] [AC:AJ133495] [PN:NRD1] [GN:nrd1]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus
ribonucleotide reductase operon.] [LE:138] [RE:536] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4709575_c2_1309	3626	7398	354	117		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4726462_f2_572	3627	7399	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4726527_f3_774	3628	7400	528	175	749	3.2e-74

Description

pir:[LN:D69868] [AC:D69868] [PN:conserved hypothetical protein ykvM]
[GN:ykvM] [CL:hypothetical protein ykvM] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184965:g2633746] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvM]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to
hypothetical proteins] [LE:45967] [RE:46464] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4773392_f2_359	3629	7401	288	95		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4775287_c3_1420	3630	7402	1008	335	238	1.3e-34

Description

sp:[LN:YBGK_ECOLI] [AC:P75745] [GN:YBGK] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 34.4 KD PROTEIN IN PHRB-NEI INTERGENIC REGION] [SP:P75745]
[DB:swissprot] >pir:[LN:G64806] [AC:G64806] [PN:ybgK protein] [GN:ybgK]
[CL:hypothetical protein HI1730] [OR:Escherichia coli] [DB:pir2]
>gp:[GI:d1036362:g4062308] [LN:D90710] [AC:D90710:AB001340] [PN:Hypothetical
protein HI1730] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA,
clone:Kohara clone #175] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA.
(15.9 - 16.3 min).] [NT:ORF_ID:o175#7; similar to PIR Accession Number]
[LE:6967] [RE:7899] [DI:direct] >gp:[GI:g1786930] [LN:AE000174]
[AC:AE000174:U00096] [PN:putative carboxylase] [GN:ybgK] [FN:putative
enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2]
[DE:Escherichia coli K-12 MG1655 section 64 of 400 of the completegenome.]
[NT:o310; This 310 aa ORF is 48 pct identical (1 gap)] [LE:10112] [RE:11044]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_47763_f3_814	3631	7403	186	61		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4804643_f1_90	3632	7404	246	81	75	0.0026

Description

gp:[GI:e1332553:g3764009] [LN:PFMAL3P4] [AC:AL008970] [GN:MAL3P4.11]
[OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
[DB:genpept-invl] [DE:Plasmodium falciparum MAL3P4, complete sequence.]
[NT:predicted using hexExon; MAL3P4.11 (PFC0510w),] [LE:68636] [RE:71146]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4806575_c2_1171	3633	7405	651	216	503	3.7e-48

Description

pir:[LN:H69854] [AC:H69854] [PN:hypothetical protein ykaA] [GN:ykaA]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181486:g2632006] [LN:BSAJ2571]
[AC:AJ002571] [PN:YkaA] [GN:ykaA] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA
and ykoR.] [LE:2613] [RE:3230] [DI:complement] >gp:[GI:e1183305:g2633639]
[LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykaA] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7
of 21): from 1194391to 1411140.] [LE:155562] [RE:156179] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4876077_f3_796	3634	7406	714	237	778	2.7e-77

Description

pir:[LN:C69868] [AC:C69868] [PN:coenzyme PQQ synthesis homolog ykvL]
[GN:ykvL] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184964:g2633745]
[LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvL] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8
of 21): from 1394791to 1603020.] [NT:similar to coenzyme PQQ synthesis]
[LE:45218] [RE:45949] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_4885876_c1_1071	3635	7407	918	305	829	1.1e-82

Description

sp:[LN:YVCJ_BACSU] [AC:O06973] [GN:YVCJ] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 33.9 KD PROTEIN IN CRH-TRXB INTERGENIC REGION] [SP:O06973]
[DB:swissprot] >pir:[LN:H70031] [AC:H70031] [PN:conserved hypothetical
protein yvcJ] [GN:yvcJ] [CL:Bacillus subtilis conserved hypothetical
protein yvcJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186165:g2635990]
[LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcJ] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins]
[SP:O06973] [LE:171011] [RE:171898] [DI:complement]
>gp:[GI:e313026:g1945650] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical
protein] [GN:yvcJ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
genomic DNA fragment (88 kb).] [NT:similar to hypothetical MTCY21B4]
[SP:O06973] [LE:9773] [RE:10660] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4892878_c3_1357	3636	7408	1077	358	455	4.5e-43

Description

gp:[GI:g1913906] [LN:SAU91741] [AC:U91741] [PN:TagX] [GN:tagX] [FN:teichoic acid biosynthesis] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus teichoic acid biosynthesis TagB gene, partialcds and TagX and TagD genes, complete cds.] [LE:632] [RE:1471] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_4898376_f2_574	3637	7409	207	68	52	0.024

Description

gp:[GI:g4588017] [LN:AF087657] [AC:AF087657] [PN:NADH-ubiquinone oxidoreductase chain 6] [GN:ND6] [OR:Mitochondrion Agrocybe aegerita] [SR:Agrocybe aegerita] [DB:genpept-pln2] [DE:Agrocybe aegerita NADH-ubiquinone oxidoreductase chain 6 (ND6)gene, mitochondrial gene encoding mitochondrial protein, completecds.] [NT:NADH dehydrogenase] [LE:34] [RE:453] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5084652_f3_849	3638	7410	507	168	536	1.2e-51

Description

gp:[GI:g1575061] [LN:SAU57060] [AC:U57060] [PN:ScdA] [GN:scdA] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus scdA gene, complete cds.] [NT:S. aureus cells containing a scdA disruption have] [LE:361] [RE:1035] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5117793_c3_1531	3639	7411	273	91	197	9.9e-16

Description

sp:[LN:YRN3_VIBPA] [AC:P46231] [OR:VIBRIO PARAHAEMOLYTICUS] [DE:HYPOTHETICAL PROTEIN IN RNT 5'REGION (ORF3) (FRAGMENT)] [SP:P46231] [DB:swissprot]
>gp:[GI:g497126] [LN:VPU06949] [AC:U06949] [PN:ORF3] [OR:Vibrio parahaemolyticus] [DB:genpept-bct1] [DE:Vibrio parahaemolyticus BB22 RNase T (rnt) gene and flagellar motorcomponent (motY) gene, complete cds.] [LE:<1] [RE:420] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5131265_c2_1243	3640	7412	276	91	80	0.0071

Description

gp:[GI:g3582235] [LN:AE001272] [AC:AE001272] [PN:L. lactis predicted coding region ORF00014] [GN:ORF00014] [OR:Lactococcus lactis] [DB:genpept-bct2] [DE:Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmidsequence.] [NT:hypothetical protein; identified by GeneMark;] [LE:10983] [RE:11600] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5182962_f1_196	3641	7413	1068	355	295	1.3e-30

Description

sp:[LN:RESE_BACSU] [AC:P35164] [GN:RESE] [OR:BACILLUS SUBTILIS] [EC:2.7.3.-] [DE:SENSOR PROTEIN RESE,] [SP:P35164] [DB:swissprot] >pir:[LN:H69691] [AC:H69691:S45560] [PN:two-component sensor histidine kinase rese] [GN:rese] [CL:sensor histidine kinase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g410142] [LN:BACDIA] [AC:L09228] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168, sub_species Marburg) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis spoVA to serA region.] [NT:ORFX18] [LE:22425] [RE:24194] [DI:direct] >gp:[GI:e1185580:g2634746] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:two-component sensor histidine kinase] [GN:rese] [FN:involved in global regulation of aerobic and] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:alternate gene name: ypxE] [SP:P35164] [LE:19389] [RE:21158] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5195393_c3_1352	3642	7414	654	217	1088	3.8e-110

Description

gp:[GI:e255543:g1617434] [LN:SESIRR] [AC:X99128] [PN:putative iron dependant repressor] [GN:sirR] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis sirR gene.] [LE:14] [RE:658] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5276677_c1_1026	3643	7415	1566	521	703	2.4e-69

Description

pir:[LN:B64622] [AC:B64622] [PN:osmoprotection protein] [OR:Helicobacter pylori] [DB:pir2] >gp:[GI:g2313949] [LN:AE000593] [AC:AE000593:AE000511] [PN:osmoprotection protein (proWX)] [GN:HP0818] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 71 of 134 of the complete genome.] [NT:similar to PID:1109685 SP:Q45461 GB:AL009126] [LE:4862] [RE:6523] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5283592_f1_215	3644	7416	288	95	73	0.014

Description

gp:[GI:g1054677] [LN:CCCOX3] [AC:X92734] [PN:cytochrome oxidase] [GN:coxIII] [OR:Mitochondrion Chara corallina] [SR:Chara corallina] [DB:genpept-pln1] [DE:C.corallina mitochondrial cox3 gene.] [NT:subunit III] [LE:<1] [RE:>381] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_5292175_c3_1484	3645	7417	1323	440	2112	1.2e-218

Description

gp:[GI:g3152725] [LN:AF065394] [AC:AF065394] [PN:enolase] [GN:eno] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus enolase (eno) gene, complete cds.] [NT:ENO; laminin binding protein] [LE:103] [RE:1407] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_53552_f2_450	3646	7418	660	219	179	8.0e-14

Description

sp:[LN:GRPB_BACFI] [AC:Q45133] [GN:GRPB] [OR:BACILLUS FIRMUS] [DE:GLUTAMATE-RICH PROTEIN GRPB] [SP:Q45133] [DB:swissprot] >gp:[GI:g1209681] [LN:BFU39410] [AC:U39410] [PN:glutamate-rich protein] [GN:grpB] [OR:Bacillus firmus] [SR:Bacillus firmus strain=OF4] [DB:genpept-bct1] [DE:Bacillus firmus OrfA, OrfB, glutamate-rich protein (grpA), OrfC, and glutamate-rich protein (grpB) genes, complete cds.] [LE:2695] [RE:3219] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_5355325_c3_1454	3647	7419	888	295	526	1.4e-50

Description

sp:[LN:DEGV_BACSU] [AC:P32436] [GN:DEGV] [OR:BACILLUS SUBTILIS] [DE:DEGV PROTEIN] [SP:P32436] [DB:swissprot] >pir:[LN:D30191] [AC:I40386:D30191:A70042:S28596] [PN:conserved hypothetical protein yviA] [GN:yviA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g39848] [LN:BSCOMFG] [AC:Z18629] [PN:U3] [GN:degUorf3] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis comF gene.] [SP:P32436] [LE:1] [RE:846] [DI:direct] >gp:[GI:e1184454:g2636074] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yviA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: degV, sacU; similar to] [LE:45634] [RE:46479] [DI:complement] >gp:[GI:g1762331] [LN:BSU56901] [AC:U56901] [GN:degV] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis putative transcriptional regulator (yvhJ),Ycr59c/YigZ homolog (yvhK), histidine kinase (degS),transcriptionalregulator of degradation enzyme (degU), (degV), (comFA), (comFB), (comFC), flagellar protein (yviB), negative regulator of flagellin(flgM), flagellar protein (yviC), flagellar-hook associated protein1 (flgK), flagellar-hook associated protein 3 (flgL), (yviE),transmembrane protein (yviF), (csrA), flagellin (hag), flagellarprotein (yviH), flagellar hook-associated protein 2 (fliD),flagellar protein (fliS), flagellar protein (fliT), sigma-54modulator homolog (yviI), and (secA) genes, complete cds.] [LE:4114] [RE:4959] [DI:direct] >gp:[GI:e1184454:g2636074] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yviA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: degV, sacU; similar to] [SP:P32436] [LE:45634] [RE:46479] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_5367843_c3_1488	3648	7420	759	252	791	1.1e-78

Description

sp:[LN:EST_BACST] [AC:Q06174] [GN:EST] [OR:BACILLUS STEAROTHERMOPHILUS] [EC:3.1.1.1] [DE:CARBOXYLESTERASE PRECURSOR,] [SP:Q06174] [DB:swissprot] >pir:[LN:JC1374] [AC:JC1374] [PN:carboxylesterase,] [GN:Est] [OR:Bacillus stearothermophilus] [EC:3.1.1.1] [DB:pir2] >gp:[GI:d1002674:g216314] [LN:BACPBH7] [AC:D12681] [PN:esterase] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus DNA, clone pBH7] [DB:genpept-bct1] [DE:Bacillus stearothermophilus esterase gene.] [LE:181] [RE:924] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_57800_c3_1494	3649	7421	147	48		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_5869433_f2_542	3650	7422	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_5869702_f2_595	3651	7423	309	102	87	0.015
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Description

sp: [LN:YMW6_YEAST] [AC:Q04264:Q04780] [GN:YMR076C:YM9582.01C:YM9916.15C]
 [OR:SACCHAROMYCES CEREVISIAE] [SR:,BAKER'S YEAST] [DE:HYPOTHETICAL 147.0 KD
 PROTEIN IN ABF2-CHL12 INTERGENIC REGION] [SP:Q04264:Q04780] [DB:swissprot]
 >pir: [LN:S54451] [AC:S54451:S52836] [PN:hypothetical protein
 YMR076c:hypothetical protein YM9582.01c:hypothetical protein YM9916.15c]
 [GN:PDS5] [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:13R]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_5938762_c1_987	3652	7424	1704	567	566	7.8e-55
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Description

sp: [LN:CYDD_HAEIN] [AC:P45082] [GN:CYDD:HI1157] [OR:HAEMOPHILUS INFLUENZAE]
 [DE:TRANSPORT ATP-BINDING PROTEIN CYDD] [SP:P45082] [DB:swissprot]
 >pir: [LN:F64186] [AC:F64186] [PN:ABC-type transport protein cydD] [GN:cydD
] [CL:unassigned ATP-binding cassette proteins: ATP-binding cassette
 homology] [OR:Haemophilus influenzae] [DB:pir2] >gp: [GI:g1574714]
 [LN:U32795] [AC:U32795:L42023] [PN:ATP-binding protein protein (cydD)]
 [GN:HI1157] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus
 influenzae Rd section 110 of 163 of the completegenome.] [NT:similar to
 GB:L21749 SP:P29018 GB:L25859 PID:146416] [LE:6353] [RE:8113]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6023915_c2_1313	3653	7425	969	322	1144	4.4e-116

Description

pir:[LN:D70023] [AC:D70023] [PN:lipoic acid synthetase, yutB] [GN:yutB]
[CL:lipoic acid synthase] [OR:Bacillus subtilis] [EC:2.8.1.-] [DB:pir2]
>gp:[GI:e1184312:g2635730] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutB]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
lipoic acid synthetase] [LE:122382] [RE:123188] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6037756_f3_682	3654	7426	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6050010_f1_177	3655	7427	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6051500_c1_972	3656	7428	189	62		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_6051537_c1_1063	3657	7429	276	91	112	1.0e-06

Description

sp:[LN:CSBA_BACSU] [AC:P37953] [GN:CSBA] [OR:BACILLUS SUBTILIS] [DE:CSBA PROTEIN] [SP:P37953] [DB:swissprot] >gp:[GI:g142780] [LN:BACCSBA] [AC:M80473] [GN:csbA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168, sub_species Marburg) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis csbA and uvr/dinA genes, complete cds.] [NT:putative membrane protein; putative] [LE:380] [RE:610] [DI:direct] >gp:[GI:g142842] [LN:BACDINA76] [AC:M64048] [PN:DNase inhibitor] [GN:dinA] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNase inhibitor (dinA76) gene, complete cds and promoter region.] [LE:64] [RE:294] [DI:direct] >gp:[GI:e1184424:g2636044] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:putative membrane protein] [GN:csbA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P37953] [LE:17086] [RE:17316] [DI:complement] >gp:[GI:g2618840] [LN:AF017113] [AC:AF017113] [PN:CsbA] [GN:csbA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:12977] [RE:13207] [DI:direct] >gp:[GI:e1184424:g2636044] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:putative membrane protein] [GN:csbA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P37953] [LE:17086] [RE:17316] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_6053176_f1_195	3658	7430	519	172		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_6056628_c3_1339	3659	7431	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6057338_c3_1518	3660	7432	840	279	622	9.1e-61

Description

pir:[LN:H70015] [AC:H70015] [PN:hypothetical protein yunE] [GN:yunE]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184317:g2635735] [LN:BSUB0017]
 [AC:Z99120:AL009126] [GN:yunE] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
 from 3197001to 3414420.] [LE:127136] [RE:127957] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6094177_c2_1235	3661	7433	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6101581_f1_74	3662	7434	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6257763_c3_1479	3663	7435	660	219	189	1.7e-13

Description

gp:[GI:g2246532] [LN:U93872] [AC:U93872] [OR:Kaposi's sarcoma-associated
 herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus
 8] [DB:genpept-vrl] [DE:Kaposi's sarcoma-associated herpesvirus glycoprotein
 M, DNA replication protein, glycoprotein, DNA replication protein,
 FLICEinhibitory protein and v-cyclin genes, complete cds, and
 tegumentprotein gene, partial cds.] [NT:ORF 73, contains large complex
 repeat CR 73] [LE:124324] [RE:127593] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_626592_c1_935	3664	7436	852	283	233	1.5e-19

Description

pir:[LN:A69463] [AC:A69463] [PN:2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hydrolase (pcbD) homolog] [OR:Archaeoglobus fulgidus] [DB:pir2]
>gp:[GI:g2648849] [LN:AE000986] [AC:AE000986:AE000782]
[PN:2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid] [GN:AF1706]
[OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 121 of 172 of the complete genome.] [NT:similar to GP:1395174 percent identity: 29.41;] [LE:11775] [RE:12491] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6423376_f3_670	3665	7437	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6437525_f3_862	3666	7438	294	97		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6440640_c3_1379	3667	7439	1278	425	139	6.0e-06

Description

pir:[LN:D71621] [AC:D71621] [PN:hypothetical protein PFB0185w] [GN:PFB0185w]
[OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g3845117] [LN:AE001378]
[AC:AE001378:AE001362] [PN:hypothetical protein] [GN:PFB0185w]
[OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
[DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.] [NT:predicted by GlimmerM] [LE:6504:8652]
[RE:8473:9075] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6444037_c2_1180	3668	7440	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6642827_c3_1342	3669	7441	2403	800	1527	1.1e-156

Description

pir:[LN:A70010] [AC:A70010] [PN:NADH dehydrogenase homolog yufT] [GN:yufT]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184238:g2635656] [LN:BSUB0017]
 [AC:Z99120:AL009126] [GN:yufT] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
 from 3197001to 3414420.] [NT:similar to NADH dehydrogenase] [LE:48758]
 [RE:51082] [DI:direct] >gp:[GI:e311455:g1934817] [LN:BSZ93937] [AC:Z93937]
 [PN:unknown] [GN:yufT] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis genomic DNA fragment from yufK to yufV.] [NT:potential Na/H
 antiporter/phaA homologue/NADH] [LE:10546] [RE:12870] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6650312_f2_600	3670	7442	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6675016_c1_1077	3671	7443	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6680312_f2_518	3672	7444	714	237	211	4.7e-17

Description

gp:[GI:g3329623] [LN:CELF36H12] [AC:AF078790] [GN:F36H12.3]
 [OR:Caenorhabditis elegans] [DB:genpept-inv2] [DE:Caenorhabditis elegans
 cosmid F36H12.] [NT:coded for by C. elegans cDNA CEMSF30F]
 [LE:21606:21872:22500:22677] [RE:21701:22454:22629:22875] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6681577_c1_1110	3673	7445	432	143	277	3.3e-24

Description

pir:[LN:G70020] [AC:G70020] [PN:hypothetical protein yusF] [GN:yusF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184356:g2635774] [LN:BSUB0017]
 [AC:Z99120:AL009126] [GN:yusF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
 from 3197001to 3414420.] [LE:167450] [RE:167890] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6695968_c2_1320	3674	7446	1470	489	2005	2.5e-207

Description

gp:[GI:g4530241] [LN:AF101234] [AC:AF101234] [PN:D-alanine-D-alanyl carrier protein ligase DltA] [GN:dltA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus dltABCD operon, complete sequence; and unknown gene.] [LE:1590] [RE:3047] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6822175_c2_1222	3675	7447	1914	637	1229	4.3e-125

Description

pir:[LN:F69901] [AC:F69901] [PN:DNA helicase recQ:ATP-dependent DNA helicase homolog yocI] [GN:yocI] [CL:recQ protein:DEAD/H box helicase homology:recQ helicase homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g2619051] [LN:AF027868] [AC:AF027868] [PN:RecQ homolog] [GN:yocI] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosome region between terC and odhAB.] [NT:similar to E.coli RecQ protein (607 aa)] [LE:74004] [RE:75779] [DI:complement] >gp:[GI:e1185394:g2634315] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yocI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [NT:similar to ATP-dependent DNA helicase] [LE:93095] [RE:94870] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6823453_c3_1346	3676	7448	483	160	270	1.8e-23

Description

gp:[GI:d1036085:g4001729] [LN:AB015981] [AC:AB015981] [PN:MnhE] [GN:mnhE] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:5474] [RE:5953] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6829638_c3_1402	3677	7449	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6833313_c3_1371	3678	7450	1920	639	550	3.9e-53

Description

pir:[LN:B70001] [AC:B70001] [PN:ABC transporter (permease) homolog ytsD]
 [GN:ytsD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185910:g2635521]
 [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsD] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 16 of 21): from 2997771to 3213410.] [NT:similar to ABC transporter
 (permease)] [LE:110708] [RE:112648] [DI:complement] >gp:[GI:g2293178]
 [LN:AF008220] [AC:AF008220] [PN:YtsD] [GN:ytsD] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
 [NT:similarity to NADH dehydrogenase] [LE:67779] [RE:69719] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6836088_c1_1118	3679	7451	1320	439	1260	2.2e-128

Description

pir:[LN:G70019] [AC:G70019] [PN:conserved hypothetical protein yurX]
 [GN:yurX] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184348:g2635766]
 [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yurX] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins]
 [LE:160723] [RE:162036] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_6929512_c1_1119	3680	7452	1416	471	2098	3.6e-217

Description

pir:[LN:D70019] [AC:D70019] [PN:conserved hypothetical protein yurU]
 [GN:yurU] [CL:Methanobacterium thermoautotrophicum ABC transporter chain
 Ycf24] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184345:g2635763]
 [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yurU] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins]
 [LE:157652] [RE:159049] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_7042878_f1_40	3681	7453	177	58		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_7239188_f2_519	3682	7454	675	224	491	6.9e-47

Description

pir:[LN:D70033] [AC:D70033] [PN:conserved hypothetical protein yvdD]
 [GN:yvdD] [CL:yeast conserved hypothetical protein YJL055w] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e1186152:g2635977] [LN:BSUB0018]
 [AC:Z99121:AL009126] [GN:yvdD] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
 from 3399551to 3609060.] [NT:similar to hypothetical proteins] [LE:158450]
 [RE:159025] [DI:complement] >gp:[GI:e313036:g1945663] [LN:BSZ94043]
 [AC:Z94043] [PN:hypothetical protein] [GN:yvdD] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).] [NT:similar
 to YJF5_YEAST hypothetical 26.9 kd protein] [LE:22646] [RE:23221]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_7800_c1_1093	3683	7455	198	65	54	0.033

Description

gp:[GI:g3789915] [LN:AF083442] [AC:AF083442] [PN:G protein-coupled receptor
 G2A] [OR:Mus musculus] [SR:house mouse] [DB:genpept-rod] [DE:Mus musculus G
 protein-coupled receptor G2A mRNA, complete cds.] [LE:147] [RE:1295]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_781415_c3_1393	3684	7456	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_783375_c2_1236	3685	7457	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_788950_c3_1347	3686	7458	531	176	219	4.6e-18

Description

pir:[LN:E70008] [AC:E70008] [PN:conserved hypothetical protein yufB]
 [GN:yufB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184243:g2635661]
 [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yufB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins]
 [LE:54068] [RE:54442] [DI:direct] >gp:[GI:e311512:g1934774] [LN:BSZ93932]
 [AC:Z93932] [PN:unknown] [GN:yufB] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis genomic DNA fragment from yufA to yufE.] [LE:7086] [RE:7460]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_821963_c2_1165	3687	7459	546	181	103	0.0018

Description

gp:[GI:g4731376] [LN:AF135127] [AC:AF135127:AF047896] [PN:isoflavone
 reductase homolog Bet v 5] [GN:BETV5] [OR:Betula pendula] [SR:European white
 birch] [DB:genpept-pln2] [DE:Betula pendula isoflavone reductase homolog Bet
 v 5 (BETV5) mRNA,partial cds.] [NT:allergen; IgE binding protein] [LE:1]
 [RE:>900] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_822777_c3_1397	3688	7460	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_870300_c1_958	3689	7461	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_899177_c3_1335	3690	7462	930	309	596	5.2e-58

pir:[LN:G70046] [AC:G70046] [PN:iron-binding protein homolog yvrC] [GN:yvrC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1249807:g2832811] [LN:BS43KBDNA]
[AC:AJ223978] [PN:putative metal binding protein, YvrC] [GN:yvrC]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA
fragment from yvsA to yvqA.] [LE:23792] [RE:24736] [DI:direct]
>gp:[GI:e1184397:g2635815] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvrC]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
iron-binding protein] [LE:205551] [RE:206495] [DI:complement]
>gp:[GI:e1186006:g2635831] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvrC]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to
iron-binding protein] [LE:3001] [RE:3945] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AR7503001001_900256_c1_1017	3691	7463	210	69		

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_959437_c1_965	3692	7464	159	52		

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_9642_f1_227	3693	7465	876	291	769	2.4e-76

pir:[LN:E70006] [AC:E70006] [PN:probable bacitracin resistance protein (undecapreno) yubB] [GN:yubB] [CL:Escherichia coli bacitracin resistance protein bacA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185988:g2635599] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:yubB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to bacitracin resistance protein] [LE:195935] [RE:196765] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_969075_c1_1109	3694	7466	354	117	359	6.7e-33

Description

pir:[LN:B70021] [AC:B70021] [PN:arsenate reductase homolog yusI] [GN:yusI]
[CL:hypothetical protein yjbd] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184359:g2635777] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusI]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
arsenate reductase] [LE:168632] [RE:168988] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_969555_f1_218	3695	7467	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_969812_f1_63	3696	7468	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_970327_c2_1301	3697	7469	297	98	167	1.5e-12

Description

pir:[LN:F70020] [AC:F70020] [PN:thioredoxin homolog yuse] [GN:yuse]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184355:g2635773] [LN:BSUB0017]
[AC:Z99120:AL009126] [GN:yuse] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
from 3197001to 3414420.] [NT:similar to thioredoxin] [LE:167128] [RE:167448]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_973400_f3_690	3698	7470	180	59	43	0.013

Description

gp:[GI:e1363550:g4127809] [LN:EFAJ3161] [AC:AJ223161] [PN:hypothetical
protein] [GN:orf6] [OR:Enterococcus faecalis] [DB:genpept-bct1]
[DE:Enterococcus faecalis plasmid pS86, rep86 and mob86 genes.] [LE:4421]
[RE:4732] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_978426_c1_1043	3699	7471	978	325	1338	1.2e-136

Description

gp:[GI:e1330452:g3724155] [LN:SAA005352] [AC:AJ005352] [PN:membrane protein]
[GN:sstA] [FN:iron transport protein] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:Staphylococcus aureus, Sst putative iron transport
operon.] [LE:273] [RE:1245] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_9882950_c2_1204	3700	7472	1350	449	1090	2.3e-110

Description

sp:[LN:YHDP_BACSU] [AC:O07585] [GN:YHDP] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 49.9 KD PROTEIN IN CITA-SSPB INTERGENIC REGION] [SP:O07585]
[DB:swissprot] >pir:[LN:F69826] [AC:F69826] [PN:hemolysin homolog yhdP]
[GN:yhdP] [CL:hypothetical protein HI0107] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182956:g2633290] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdP]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to
hemolysin] [SP:O07585] [LE:32043] [RE:33377] [DI:complement]
>gp:[GI:e1191881:g2226211] [LN:BSY14082] [AC:Y14082] [PN:hypothetical
protein] [GN:yhdP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.]
[NT:Similarity to yhdT, this submission, and to] [SP:O07585] [LE:18691]
[RE:20025] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_9884625_f2_464	3701	7473	1509	502	1226	9.0e-125

Description

sp:[LN:YCLF_BACSU] [AC:P94408] [GN:YCLF] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION] [SP:P94408]
[DB:swissprot] >pir:[LN:C69762] [AC:C69762] [PN:di-tripeptide ABC
transporter (membrane pr) homolog yclF] [GN:yclF] [CL:peptide transporter
protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182334:g2632668]
[LN:BSUB0003] [AC:Z99106:AL009126] [GN:yclF] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3
of 21): from 402751 to611850.] [NT:similar to di-tripeptide ABC transporter
(membrane)] [SP:P94408] [LE:13065] [RE:14543] [DI:complement]
>gp:[GI:d1009635:g1805438] [LN:D50453] [AC:D50453] [PN:homologue of
Di-tripeptide transporter Dtp of L.] [GN:yclF] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus
subtilis DNA for 25-36 degree region containing theamyE-srfA region,
complete cds.] [LE:95468] [RE:96946] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_14507827_c3_220	3706	7478	168	55	273	8.7e-24

Description

pir:[LN:F56976] [AC:F56976] [PN:transfer complex protein TrsO']
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g3676448] [LN:AF051917]
 [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus]
 [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
 sequence.] [NT:Orf55; possibly truncated by IS257 transposon] [LE:37179]
 [RE:37346] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_14844187_c2_195	3707	7479	3081	1026	5411	0.0

Description

sp:[LN:SYIP_STAAU] [AC:P41368] [GN:MUPR] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:6.1.1.5] [DE:(ISOLEUCINE--TRNA LIGASE) (ILERS) (MUPIROCIN RESISTANCE
 PROTEIN)] [SP:P41368] [DB:swissprot] >gp:[GI:g581558] [LN:SADNAMUPR]
 [AC:X75439] [PN:isoleucyl tRNA synthetase] [GN:ileS] [OR:Staphylococcus
 aureus] [DB:genpept-bct1] [DE:S.aureus plasmid encoded DNA, mup R gene.]
 [SP:P41368] [LE:477] [RE:3551] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_15631901_c3_234	3708	7480	645	214	943	8.8e-95

Description

gp:[GI:g3676416] [LN:AF051917] [AC:AF051917:L19570] [PN:putative resolvase
 Res] [GN:res] [OR:Staphylococcus aureus] [DB:genpept-bct2]
 [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:2779]
 [RE:3336] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_156910_f2_62	3709	7481	483	160	729	4.2e-72

Description

gp:[GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [NT:Orf149] [LE:2068] [RE:2484]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_19625062_c3_225	3710	7482	165	54		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_19665885_c1_175	3711	7483	1728	575	2999	0.0
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Description

gp:[GI:g3676419] [LN:AF051917] [AC:AF051917:L19570] [PN:LtrC-like protein]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf575; similar to Lactococcus lactis
pRS01 LtrC] [LE:6350] [RE:8074] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_19744010_c3_232	3712	7484	288	95	466	3.1e-44
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Description

gp:[GI:g3676414] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf423] [LE:755] [RE:2026]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_2115625_f2_61	3713	7485	195	64		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_2150037_c1_180	3714	7486	336	111	464	5.0e-44
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Description

gp:[GI:g3676421] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf90] [LE:10316] [RE:10588]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_21754035_f3_110	3715	7487	141	46		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_23468753_c3_236	3716	7488	1647	548	2838	1.4e-295
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Description

gp:[GI:g3676418] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf538] [LE:4531] [RE:6147]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_23594712_c2_211	3717	7489	309	102	392	2.1e-36
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Description

gp:[GI:g3676422] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane
protein] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
aureus plasmid pSK41, complete sequence.] [NT:Orf77] [LE:10692] [RE:10925]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_23603382_c2_196	3718	7490	603	200	688	9.2e-68
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Description

sp:[LN:YIL2_STAAU] [AC:P41370] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL
PROTEIN IN ILES 3'REGION (ORF C) (FRAGMENT)] [SP:P41370] [DB:swissprot]
>pir:[LN:S40262] [AC:S40262] [PN:hypothetical protein C] [OR:Staphylococcus
aureus] [DB:pir2] >gp:[GI:g438228] [LN:SADNAMUPR] [AC:X75439]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid encoded
DNA, mup R gene.] [NT:ORF C] [SP:P41370] [LE:3621] [RE:>4013] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23651712_c2_191	3719	7491	480	159	779	2.1e-77

Description

pir:[LN:B56976] [AC:B56976] [PN:transfer protein complex TrsJ] [GN:trsJ]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310617] [LN:STATRSC]
[AC:L11998] [GN:trsJ] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
conjugative transfer gene complex (trs).] [NT:putative] [LE:10014]
[RE:10478] [DI:direct] >gp:[GI:g3676444] [LN:AF051917] [AC:AF051917:L19570]
[PN:putative membrane protein TraJ] [GN:traJ] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
sequence.] [LE:33617] [RE:34081] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23727302_c3_215	3720	7492	1296	431	2175	2.5e-225

Description

pir:[LN:G36891] [AC:G36891] [PN:transfer complex protein TrsF] [GN:trsF]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310613] [LN:STATRSC]
[AC:L11998] [GN:trsF] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
conjugative transfer gene complex (trs).] [NT:putative] [LE:5011] [RE:6291]
[DI:direct] >gp:[GI:g3676440] [LN:AF051917] [AC:AF051917:L19570]
[PN:putative membrane protein TraF] [GN:traF] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
sequence.] [LE:28614] [RE:29894] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23959802_c2_201	3721	7493	234	77		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23959802_f1_16	3722	7494	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23959802_f1_32	3723	7495	135	44		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23959802_f1_51	3724	7496	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23959802_f2_70	3725	7497	174	57		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_23959802_f3_119	3726	7498	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_24001537_c2_187	3727	7499	750	249	1184	2.5e-120
<u>Description</u>						

pir:[LN:E36891] [AC:E36891] [PN:transfer complex protein TrsD] [GN:trsD]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310611] [LN:STATRSC]
 [AC:L11998] [GN:trsD] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 (individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
 conjugative transfer gene complex (trs).] [NT:putative] [LE:2283] [RE:2966]
 [DI:direct] >gp:[GI:g3676438] [LN:AF051917] [AC:AF051917:L19570] [PN:TraD]
 [GN:traD] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
 aureus plasmid pSK41, complete sequence.] [LE:25886] [RE:26569] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_24298387_c1_171	3728	7500	147	48	68	0.045

Description

sp:[LN:PSBH_CHLVU] [AC:P56323] [GN:PSBH] [OR:CHLORELLA VULGARIS]
[DE:PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN] [SP:P56323] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_24393803_f1_28	3729	7501	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_24415937_c2_189	3730	7502	489	162	819	1.2e-81

Description

pir:[LN:I36891] [AC:I36891] [PN:transfer complex protein TrsH] [GN:trsH]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310615] [LN:STATRSC]
[AC:L11998] [GN:trsH] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
conjugative transfer gene complex (trs).] [NT:putative] [LE:7395] [RE:7880]
[DI:direct] >gp:[GI:g3676442] [LN:AF051917] [AC:AF051917:L19570]
[PN:lipoprotein TraH] [GN:traH] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:signal
peptide recognized as a pheromone by the] [LE:30998] [RE:31483] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_24664812_c1_155	3731	7503	423	140	671	5.8e-66

Description

pir:[LN:D36891] [AC:D36891] [PN:transfer complex protein TrsC] [GN:trsC]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310610] [LN:STATRSC]
[AC:L11998] [GN:trsC] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
conjugative transfer gene complex (trs).] [NT:putative] [LE:1889] [RE:2296]
[DI:direct] >gp:[GI:g3676437] [LN:AF051917] [AC:AF051917:L19570]
[PN:putative membrane protein TraC] [GN:traC] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
sequence.] [LE:25492] [RE:25899] [DI:direct]

Description

AI7503012391_24792033_c2_192	3733	7505	138	45
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Description

NO-HIT

AI7503012391_25587777_f1_52	3734	7506	264	87	444	6.6e-42
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Description

gp:[GI:g3676425] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf86] [LE:12564] [RE:12824]
[DI:complement]

AI7503012391_26594052_c1_150	3735	7507	336	111	567	6.1e-55
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Description

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gp:[GI:g3676424] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf109] [LE:12231] [RE:12560]
[DI:direct]
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AI7503012391_26600927_c2_206	3736	7508	786	261	1347	1.4e-137
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Description

gp:[GI:g3676417] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf259] [LE:3618] [RE:4397]
[DI:direct]

AI7503012391_29558262_c2_205	3737	7509	129	42
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NO-HIT

AI7503012391_30273550_c1_162	3738	7510	432	143	671	5.8e-66
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pir:[LN:E56976] [AC:E56976 ] [PN:transfer complex protein TrsM] [GN:trsM ]
[CL:single-stranded DNA-binding protein homology] [OR:Staphylococcus aureus]
[DB:pir2] >gp:[GI:g310620] [LN:STATRSC] [AC:L11998] [GN:trsM]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual_isolate
pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer
gene complex (trs.)] [NT:putative] [LE:13127] [RE:13519] [DI:direct]
>gp:[GI:g3676447] [LN:AF051917] [AC:AF051917:L19570] [PN:putative
single-stranded DNA binding protein] [GN:traM] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
sequence.] [LE:36730] [RE:37122] [DI:direct]

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AI7503012391_30503392_c2_188	3739	7511	1083	360	1889	5.0e-195
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gp:[GI:g3676441] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein TraG] [GN:traG] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:29912] [RE:30988] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_33786251_c3_230	3740	7512	1113	370	1926	6.0e-199

Description

sp:[LN:AACA_STAAU] [AC:P14507] [GN:AACA-APHD] [OR:STAPHYLOCOCCUS AUREUS:ENTEROCOCCUS FAECALIS] [SR:,STREPTOCOCCUS FAECALIS] [EC:2.3.1.-:2.7.1.-] [DE:AMINOGLYCOSIDE PHOSPHOTRANSFERASE, (APH(2'))] [SP:P14507] [DB:swissprot] >pir:[LN:S26353] [AC:S26353] [PN:aminoglycoside resistance protein aacA-aphD] [OR:Staphylococcus aureus] [DB:pir2] >pir:[LN:A26048] [AC:A26048] [PN:aminoglycoside acetyltransferase] [OR:Enterococcus faecalis] [DB:pir2] >gp:[GI:g152948] [LN:STAAGLSRA] [AC:M18086:M29261] [PN:aminoglycoside resistance protein] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain SK982) DNA] [DB:genpept-bct1] [DE:S.aureus transposon 4001 aacA-aphD aminoglycoside resistance gene,complete cds, and right and left IS256 transposase genes.] [LE:1725] [RE:3164] [DI:direct] >gp:[GI:g153586] [LN:STRBRP] [AC:M13771] [OR:Enterococcus faecalis] [SR:S.faecalis DNA, clone pSF815A] [DB:genpept-bct1] [DE:Streptococcus faecalis 6'-aminoglycoside acetyltransferasephosphotransferase (AAC(6')-APH(2')) bifunctional resistanceprotein, complete cds.] [NT:AAC(6')-APH(2') bifunctional resistance protein] [LE:304] [RE:1743] [DI:direct] >gp:[GI:g3676454] [LN:AF051917] [AC:AF051917:L19570] [PN:bifunctional aminoglycoside modifying enzyme] [GN:aacA-aphD] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:42505] [RE:43944] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_33786251_f2_66	3741	7513	390	129	644	4.2e-63

Description

sp:[LN:TRA6_STAAU] [AC:P19775] [GN:TNP] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS256 IN TRANSPOSON TN4001] [SP:P19775] [DB:swissprot] >pir:[LN:JS0296] [AC:JS0296] [PN:transposase] [GN:tnp] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g152947] [LN:STAAGLSRA] [AC:M18086:M29261] [PN:transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain SK982) DNA] [DB:genpept-bct1] [DE:S.aureus transposon 4001 aacA-aphD aminoglycoside resistance gene,complete cds, and right and left IS256 transposase genes.] [LE:102] [RE:1274] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_34242300_c1_158	3742	7514	2037	678	3430	0.0

Description

pir:[LN:F36891] [AC:F36891] [PN:transfer complex protein TrsE]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310612] [LN:STATRSC]
 [AC:L11998] [GN:trsE] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 (individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
 conjugative transfer gene complex (trs).] [NT:putative] [LE:2981] [RE:4999]
 [DI:direct] >gp:[GI:g3676439] [LN:AF051917] [AC:AF051917:L19570]
 [PN:putative ATPase TraE] [GN:traE] [OR:Staphylococcus aureus]
 [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
 sequence.] [LE:26584] [RE:28602] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_34642562_c1_174	3743	7515	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_35397177_c2_182	3744	7516	1062	353	1760	2.3e-181

Description

gp:[GI:g3676423] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [NT:Orf346] [LE:11188] [RE:12228]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_35397177_c3_241	3745	7517	132	44	142	3.1e-09

Description

gp:[GI:g3676423] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [NT:Orf346] [LE:11188] [RE:12228]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_36048212_c3_221	3746	7518	774	257	783	7.9e-78

Description

sp:[LN:YIL1_STAAU] [AC:P41369] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL PROTEIN IN ILES 5'REGION (ORF B) (FRAGMENT)] [SP:P41369] [DB:swissprot]
 >pir:[LN:S40261] [AC:S40261] [PN:hypothetical protein B] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g438227] [LN:SADNAMUPR] [AC:X75439]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid encoded DNA, mup R gene.] [NT:ORF B] [SP:P41369] [LE:<1] [RE:450] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_36605260_c1_169	3747	7519	630	209	1077	5.5e-109

Description

gp:[GI:g3676413] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf204] [LE:72] [RE:686] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_3907943_f3_103	3748	7520	2010	669	3498	0.0

Description

gp:[GI:g3676420] [LN:AF051917] [AC:AF051917:L19570] [PN:oriT nickase Nes]
 [GN:nes] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:8115] [RE:10112]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_3908407_c3_214	3749	7521	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_4300002_c1_153	3750	7522	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_4428802_f2_57	3751	7523	168	55		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_4486075_c1_154	3752	7524	975	324	1640	1.2e-168
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Description

pir:[LN:B36891] [AC:B36891] [PN:transfer complex protein TrsA] [GN:trsA]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310608] [LN:STATRSC]
 [AC:L11998] [GN:trsA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 (individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
 conjugative transfer gene complex (trs).] [NT:putative] [LE:521] [RE:1495]
 [DI:direct] >gp:[GI:g3676435] [LN:AF051917] [AC:AF051917:L19570] [PN:TraA]
 [GN:traA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
 aureus plasmid pSK41, complete sequence.] [LE:24124] [RE:25098] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_4586062_c1_176	3753	7525	141	46		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503012391_4724035_c1_170	3754	7526	1134	377	1728	5.7e-178
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Description

gp:[GI:g3676414] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [NT:Orf423] [LE:755] [RE:2026]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_4745437_c2_190	3755	7527	2118	705	3603	0.0

Description

pir:[LN:A56976] [AC:A56976] [PN:transfer complex protein TrsI] [GN:trsI]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310616] [LN:STATRSC]
[AC:L11998] [GN:trsI] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
conjugative transfer gene complex (trs).] [NT:putative] [LE:7896] [RE:9998]
[DI:direct] >gp:[GI:g3676443] [LN:AF051917] [AC:AF051917:L19570]
[PN:putative topoisomerase TraI] [GN:traI] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
sequence.] [LE:31499] [RE:33601] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_5109675_c2_186	3756	7528	324	107	535	1.5e-51

Description

pir:[LN:C36891] [AC:C36891] [PN:transfer complex protein TrsB] [GN:trsB]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310609] [LN:STATRSC]
[AC:L11998] [GN:trsB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
conjugative transfer gene complex (trs).] [NT:putative] [LE:1512] [RE:1829]
[DI:direct] >gp:[GI:g3676436] [LN:AF051917] [AC:AF051917:L19570]
[PN:putative membrane protein TraB] [GN:traB] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete
sequence.] [LE:25115] [RE:25432] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_5314202_c3_219	3757	7529	918	305	1524	2.4e-156

Description

pir:[LN:D56976] [AC:D56976] [PN:transfer complex protein TrsL] [GN:trsL]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310619] [LN:STATRSC]
[AC:L11998] [GN:trsL] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(individual_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
conjugative transfer gene complex (trs).] [NT:putative] [LE:12193]
[RE:13110] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_6929686_c1_152	3758	7530	693	230	1199	6.5e-122

Description

gp:[GI:g1762100] [LN:SEU40385] [AC:U40385] [PN:transposase] [GN:tnp]
[OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphyloccous
epidermidis plasmid pSK818 insertion sequenceIS257(818B) putative
transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57]
[RE:731] [DI:direct] >gp:[GI:g1762102] [LN:SEU40386] [AC:U40386]
[PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1]
[DE:Staphyloccous epidermidis plasmid pSK818 insertion sequenceIS257(818C)
putative transposase gene, complete cds.] [NT:Tnp; putative transposase]
[LE:57] [RE:731] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_6929686_c1_163	3759	7531	693	230	1201	4.0e-122

Description

pir:[LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46597] [LN:SAIS2571]
[AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.]
[LE:188] [RE:862] [DI:direct] >gp:[GI:g3676452] [LN:AF051917]
[AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_6929686_c1_168	3760	7532	693	230	1205	1.5e-122

Description

pir:[LN:C60634] [AC:C60634:S26351] [PN:probable transposase]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46600] [LN:SAIS2572]
[AC:X53951] [PN:putative transposase] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences
IS257-2, IS257-3and IS256.] [LE:1752] [RE:2426] [DI:direct]
>gp:[GI:g3676456] [LN:AF051917] [AC:AF051917:L19570] [PN:putative
transposase TnpG] [GN:tnpG] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:45713]
[RE:46387] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_6929686_c2_197	3761	7533	660	219	1116	4.1e-113

Description

pir:[LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46597] [LN:SAIS2571]
 [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.]
 [LE:188] [RE:862] [DI:direct] >gp:[GI:g3676452] [LN:AF051917]
 [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_6929686_c3_229	3762	7534	693	230	1201	4.0e-122

Description

pir:[LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46597] [LN:SAIS2571]
 [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.]
 [LE:188] [RE:862] [DI:direct] >gp:[GI:g3676452] [LN:AF051917]
 [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503012391_6929686_f3_115	3763	7535	684	227	1196	1.4e-121

Description

pir:[LN:B60634] [AC:B60634:S26350] [PN:probable transposase]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46599] [LN:SAIS2572]
 [AC:X53951] [PN:putative transposase] [OR:Staphylococcus aureus]
 [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences
 IS257-2, IS257-3and IS256.] [LE:556] [RE:1221] [DI:complement]
 >gp:[GI:g3676455] [LN:AF051917] [AC:AF051917:L19570] [PN:putative
 transposase TnpF] [GN:tnpF] [OR:Staphylococcus aureus] [DB:genpept-bct2]
 [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:44517]
 [RE:45182] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012391_822802_c3_213	3764	7536	1011	336	1647	2.2e-169

Description

gp:[GI:g3676426] [LN:AF051917] [AC:AF051917:L19570] [PN:putative replication initiation protein Rep] [GN:rep] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:13205] [RE:14164] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012392_1442583_c1_19	3765	7537	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012392_1442583_c3_25	3766	7538	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012392_23671885_c1_18	3767	7539	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012392_2776391_f3_12	3768	7540	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503012392_29323431_f3_15	3769	7541	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503012392_30495306_f2_6	3770	7542	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503012392_34023375_c2_23	3771	7543	501	166	790	1.4e-78

Description

sp:[LN:REMA_STAAU] [AC:P13969] [GN:REPL:REP] [OR:STAPHYLOCOCCUS AUREUS:STAPHYLOCOCCUS SIMULANS] [DE:REPLICATION AND MAINTENANCE PROTEIN (PLASMID REPLICATION PROTEIN)] [SP:P13969] [DB:swissprot] >pir:[LN:A29827] [AC:A29827:C46568] [PN:replication protein REP] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g153064] [LN:PE5PE5A] [AC:M17990] [GN:repL] [OR:Plasmid pE5] [SR:Plasmid pE5 DNA] [DB:genpept-bct1] [DE:Plasmid pE5 (from Staphylococcus aureus, strain RN451) repL proteinand ermC protein, complete cds.] [LE:389] [RE:865] [DI:direct] >gp:[GI:g506624] [LN:STAPT48CG] [AC:M19652] [OR:Plasmid pT48] [SR:Plasmid pT48 (from S.aureus strain T48) DNA] [DB:genpept-bct1] [DE:Plasmid pT48 (from S.aureus strain T48) complete genome.] [NT:putative. ORF B.] [LE:64] [RE:540] [DI:complement] >gp:[GI:g2407672] [LN:AF019140] [AC:AF019140] [PN:Rep] [GN:rep] [OR:Staphylococcus simulans] [DB:genpept-bct2] [DE:Staphylococcus simulans erythromycin resistance plasmid pPV142 rRNAN-6-methyltransferase (ermM) and replication protein (rep) genes,complete cds.] [NT:plasmid replication protein] [LE:1699] [RE:2175] [DI:direct] >gp:[GI:g1791222] [LN:SCU82607] [AC:U82607] [PN:plasmid replication protein] [OR:Staphylococcus chromogenes] [DB:genpept-bct2] [DE:Staphylococcus chromogenes plasmid pPV141 erythromycin resistanceplasmid, rRNA N-6-methyltransferase (ermM) and plasmid replicationprotein genes, complete cds.] [LE:1583] [RE:2059] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503012392_4304683_c2_21	3772	7544	771	256	1270	2.0e-129

Description

sp:[LN:ERM4_STAAU] [AC:P13978] [GN:ERMC] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.1.1.48] [DE:RESISTANCE PROTEIN)] [SP:P13978] [DB:swissprot] >pir:[LN:B46568] [AC:B46568] [PN:ermC protein] [CL:rRNA (adenine-N6-)-methyltransferase] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g455358] [LN:STAPT48CG] [AC:M19652] [PN:23S RNA methylase] [GN:ermC] [OR:Plasmid pT48] [SR:Plasmid pT48 (from S.aureus strain T48) DNA] [DB:genpept-bct1] [DE:Plasmid pT48 (from S.aureus strain T48) complete genome.] [LE:988] [RE:1722] [DI:complement]